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Maximum DB
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Maximum Match 100%
Listing first 45 summaries
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 SIKRDHNDYSKNPM 14
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# ALIGNMENTS

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 C;Accession: PC1232

copia polyprotein - fruit fly (Drosophila simulans) retrotransposon copia (fragments) C/Species: Drosophila simulans

#text\_change 19-Feb-1999

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A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-1409 «MOU»
A;Rossidues: GB:M11240; NID:g158615; PIDN:AAA74497.1; PID:g950318
A;Cross-references: GB:M11240; NID:g158615; PIDN:AAA74497.1; PID:g950318
A;Miller, K.; Rosenbaum, J.; Zbrzezna, V.; Pogo, A.O.
Nucleic Acids Res. 17, 2134, 1989
Nucleic Acids Res. 17, 2134, 1989
A;Title: The nucleotide sequence of Drosophila melanogaster copia-specific 2.1-kb mRNA.
A;Title: The number: S03612; MUID:89183629; PMID:2538806
A;Accession: S03612; MUID:89183629; PMID:2538806
A;Accession: S03612
                                                                                                                                                                                                                                                                                copia polyprotein - fruit fly (Drosophila melanogaster) retrotransposon copia N;Contains: copia protein, 31K; copia protein, 48K; proteinase C;Species: Drosophila melanogaster C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 16-Jul-1999 C;Accession: A03324; 803612; S14835 R;Mount, S.M.; Rubin, G.M.

Mol. Ceil. Biol. 5, 1630-1638, 1985 Mol. Ceil. Biol. 5, 1630-1638, 1985 A;Reference number: A03324; MUID:85267679; PMID:2410772 A;Accession: A03324; MUID:85267679; PMID:2410772
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A;Mobile element: retrotransposon copia
C;Superfamily: retrovirus-related polyprotein
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A;Residues: 1-313;314-787 <YOS>
A;Cross_references: DDBJ:D10880
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A;Title: Efficient amplification of Drosophila simulans copia directed by high-level re
A;Reference number: PC1232) MUID:93013034; PMID:1383092
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Molecule type: mRNA;Residues: 1-391,1375-1409
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9; Conservat
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69.2%;
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Pred. No.
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galactosamine-containing minor teichoic acid biosynthesis ggaB - Bacillus subtilis C;Species: Bacillus C; Bacillus C;
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A;Title: Virus-11ke particle formation of Drosophila copia through autocatalytic A;Reference number: S14835; MUID:90151630; PMID:1689241
A;Accession: S14835
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A;Reference number: Z21829
A;Accession: T39116
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A;Residues: 1-391,1375-1409 <YOS>
A;Cross-references: EMBL:X54147; NID:g7749; PIDN:CAA38086.1; PID:g7750
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A; Residues: 1-840 < HUN>
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R;Yoshioka, K.; Honma, H.; Zushi, M.; Kondo, S.; Togashi, S.; Miyake, T.; Shiba,
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Best Local
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9; Conserva
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ilarity 69.2%;
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Pred. No.
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A;Molecule type: DNA
A;Residues: 1-202 <OLL>
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A; Accession: T36368
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                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL049628; PIDN:CAB40857.1; GSPDB:GN00070; SCOEDB:SCE94.08
A;Experimental source: strain A3(2)
                                                                                                  Best
                                                                                                                                  Query Match
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Local

l Similarity 7; Conserv

Conservative

0

Mismatches

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Indels

0

Gaps

0

51.3%; 87.5%;

Score 40; DB Pred. No. 18;

2

Length

SCOEDB:SCE94.08

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akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: G97809
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A;Residues: 1-900 <KUN>
A;Cross-references: GB:Z99122; GB:AL009126; NID:g2636029; PIDN:CAB15585.1; PID:e1184474;
A;Experimental source: strain 168
hypothetical protein SCE94.08 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T35368 C;Accession: T35368 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajans submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation
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C;Superfamily: preprotein
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                                                                                                                                                 T36368
                                                                                                                                                                       RESULT 6
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A;Molecule type: DNA
A;Residues: 1-906 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Rickettsia conorii
;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001;Accession: G97809
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Pred. No.
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probable transcription regulator - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999 C;Accession: T36881
                                                                                           trans-Golgi membrane protein p230 - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: F64662
R;Tomb, J.F.; White, O.: Kerlavace % p. Clarker
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A;Reference number: Z21617
A;Accession: T36881
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F64662
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A; Residues: 1-548 < MUR>
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A; Residues: 1-383 < KLE>
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
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                 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKerson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 7
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Matches 7
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;Species: Borrelia burgdorferi (Lyme disease spirochete)
;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 15-Jun-2001
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Fraser, C.M.; Casjens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:AL109848; PIDN:CAB52842.1; GSPDB:GN00070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCOEDB:SCI51.18
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E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith,
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Pred. No.
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  A;Gene:
C;Superf
C;Keywor
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; De, R;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; Y.; P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Authors; Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; J. A;Authors; Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; J. A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Accession: F98025
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                             prephenate dehydrogenase (EC 1.3.1.12) [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 17-Feb-2003 C;Accession; F98025 C;Accession; F98025 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHo
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                                                                       A;Cross-references: GB:AE007317; C;Genetics:
                                                                                                                        A; Molecule type: DNA
A; Residues: 1-367 < KUR>
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                           Superfamily:
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ly: prephenate dehydrogenase, oxidoreductase

feedback

inhibition-sensitive

PIDN: AAL 00035.1;

PID:g15458868; GSPDB:GN00174

DeHoff, B; McAhren,

W

(strain

Jaskunas,

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A;Status, r--
A;Molecule type: DNA
A;Mesidues; 1-759 <TOM>
A;Residues; 1-759 <TOM>
A;Residues; GB;AE000620; GB;AE000511;
                                                                                                                                                        R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; mson, T.; Hickey, E.K.; Holt, I.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: The complete genome sequence of the gastric pathogen Helicobacter pylori A,Reference number: A64520; MUID:97394467; PMID:9252185 A,Accession: F64662
                                                                                                                                A;Gene: SP1373
C;Superfamily: prephenate
                                                                                                                                                                                                                                                                    A; Reference number: A95000;
A; Accession: F95159
                                                                                                                                                                                                                                                                                   A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                      Science 293, 498-506,
                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change
C;Accession: F95159
                                                                                                                                                                                                                                                                                                                                                                                                                                          prephenate
C;Species:
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                                                              Query Match
Best Local S
Matches 7
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Matches
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Streptococcus pneumoniae
21
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8; Conser
                                                                Similarity 7; Conserv
                               IKRDHNDY
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                                                                                                                                  dehydrogenase, feedback inhibition-sensitive
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Pred. No.
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Pred. No. 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (strain
                                                                                                                                                                                                                                                                                                                                                                          T.D.; Peterson, S.; Hei Radune; D.; Holtzapple,
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Ritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Rocression. Coscin.
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D90528
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A;Cross-references: GB:AL445566; PID:gl4089545; PIDN:CAC13305.1; GSPDB:GN00153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein MYPU_1320 [imported] - Mycoplasma pulmonis (strain UAB C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               片
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: D90528
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A; Residues: 1-412 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Accession: D90528;Chambaud, I.; Hei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Molecule type: DNA
                                                                                                                                                                                                                                                                            ;Reference number: A86141;
;Accession: C96816
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Best Local
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6; Conserve
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 SLHADFDDYSKTP 328
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Pred. No. 57;
2; Mismatches
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Pred. No.
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Pred. No. 50;
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57;
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Maiti, R.; Marziali
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R;Kitamura, A.; Takahashi, K.; Okajima, A.; Kitamura, N. Eur. J. Blochem. 224, 877-883, 1994
A;Title: Induction of the human gene for p44, a hepatitis-C-associated microtubular aggr. A;Reference number: S48218; MUID:95010078; PMID:7925411
A;Accession: S48218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:D90034
R;Honda, Y.; Kondo, J.; Maeda, T.; Yoshiyama, Y.; Yamada, E.; Shimizu, Y.K.; Shikata, T.
J. Gen. Virol. 71, 1999-2004, 1990
A;Title: Isolation and purification of a non-A, non-B hepatitis-associated microtubular
A;Reference number: A43677; MUID:91011345; PMID:2170569
A;Accession: A43677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              944 hepatitis-associated antigen - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text_change 07-May-1999
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text_change 07-May-1999
C;Accession: A43676; A43677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Cloning, sequencing and expression in Escherichia coli of cDNA for a non-A, non A,Reference number: A43676; MUID:91011346; PMID:2170570
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J. Gen. Virol. 7
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C;Date: 15-U11-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
                                                                                                                                                                                                                                                                                                                                                                                                                              microtubular aggregate protein - human
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A;Residues: 14-22;108-128;200-214;231-240 <HON>
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A;Molecule type: DNA
A;Residues: 1-444 <KIT>
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7; Conserv
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SIKLNHHDYIDSP 298
                                            SIKRDHNDYSKNP 13
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Search completed: March 22, 2004, 07:01:17 Job time: 3.91051 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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LSB5_YEANE
LSB5_YEANE
LSB5_YEANE
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VATE CITUI
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MURE WIGHR
P44 PANTR
SELB METJA
SMC4_YEAST
MPPA_SOLTU
COX2_PARPR
GTP1_BUFBU
OXA2_STRAPR
GTP1_BUFBU
OXA2_STRAPR
GTP1_BUFBU
COX2_PARPR
GTP1_BUFBU
COX2_PARPR
GTP1_BUFBU
COX2_PANTR
CHICK
SOX8_HUMAN
SX10_HUMAN
SX10_RAT
SOX8_CHICK
MURE_SUCAP
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Q05278 mycobacteri
Q64202 mycobacteri
Q91616 xenopus lae
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           P12250
P48434
O85298
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -		-!- SIMILARITY: Contains 1 CCHC-type zinc finger.	IsoId=P04146-2; Sequence=VSP_005226;		IsoId=P04146-1; Sequence=Displayed;	EVent=Alternative spliting; Named isoforms=2;	E PRODUCTS:	EMBO J. 9:535-541(1990)	sing.";	"Virus-like particle formation of Drosophila copia through		a H., Zushi	MEDLINE=90151630; PubMed=1689241;	SEQUENCE FROM N.A. (ISOFORM SHORT), AND MUTAGENESIS OF ASF-292.		Nucleic Acids Res. 17:2134-2134(1989).		"The midleotide semience of Drosophila melanogaster copia-specific	E=89183629; PubMed=2538806;	SEQUENCE FROM N.A. (ISOFORM SHORT).		VITUE-TIME DATCHCHES.;	es of copia and copia-related	T., Kanaya S., Inouye S., Yuki S., Saigo K.;	85240569; PubMed=2409449;	SEQUENCE FROM N.A., SEQUENCE OF 2-10, AND ALTERNATIVE SPLICING.			etroviral proteins.";	lete nucleoti		OBCOBNED FROM N.A. (190FORM LONG). MEDITURE ACCORDAGE DIMMONISTRATIONS.	TECHNON IN MORE	NCBI_TaxID=7227;	sophilidae; Drosophila.	ptera; Brachycera; Muscomorpha;	Metazoa, Arthropoda	Drosophila melanogaster (Fruit flv).	COUTA	Copia protein (Contains: Copia VLF protein; Copia protease	. 41, Last annotation update)	. 40, Last sequence up	reated)	P04146: 003728: 024280: 024555: 024585: 024586: 024587;		LT 1

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01-MAY-1992 (Rel. 22, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                 YEAST
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EMBL; X02599; CAA26444.1; -...
EMBL; X02599; CAA26445.1; -...
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EMBL; X02600; CAA26447.1;
EMBL; X13719; CAA31997.1;
EMBL; X54147; CAA38086.1;
                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
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InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR001584; Rve.
InterPro; IPR001878; Znf_CCHC.
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SFYGIQRDRTQ (IN VARIANT COPIA-RELATED).
MISSING (IN VARIANT COPIA-RELATED).
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N (IN REF. 2; CAA26447).
V (IN REF. 2; CAA26447).
E (IN REF. 2; CAA26447).
                                                                                                   Kleinhans U.,
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RA Alberghina L., Alexandraki D., Antoine G., Anwar R., Ballesta J.P.G., RA Benit P., Berben G., Bergantino E., Biteau N., Bolle P.-A., RA Benit P., Berben G., Bergantino E., Biteau N., Bolle P.-A., RA Benit P., Berben G., Bergantino E., Biteau N., Bolle P.-A., RA Benit P., Berben G., Bergantino E., Biteau N., Bolle P.-A., RA Bolotin-Pukuhara M., Brown A.J.P., Brown R., Buhler J.-M., RA Carignani G., Chanet R., Contreras R., Crouzet M., Daignan-Fornier B., RA Dujon B., Duesterhoeft A., Erdmann D., Demolder J., Doira C., Dubois B., RA Dujon B., Duesterhoeft A., Erdmann D., Esteban M., Fabre F., RA Dujon B., Duesterhoeft A., Erdmann D., Esteban M., Fabre F., RA Fairhead C.A., Faye G., Feldmann H., Fiers W., RA Francingues-Gaillard M.-C., Franco L., Frontali L., Fukuhara H., RA Friers M., Grenson M., Grisanti P., Grivell L.A., Haasemann M., RA Hatat D., Hegemann J.H., Herbert C.J., Hilger F., Hohmann S., Martegore C.P., Huse K., Iborra F., Indge K.J., Isono K., Jackman P., RA Hatat D., Hegemann J.H., Herbert C.J., Hilger F., Hohmann S., Lucchini G., Lutzenkirchen K., Maarte C., Van der Linden C.G., RA Lucchini G., Lutzenkirchen K., Maarte C., Wannhaupt G., Wanzano M.E., RA Martegani E., Mathieu A., Maurer C.T.C., McConnell D., McKee R.A., RA Messenguy F., Mewes H.-W., Molemans F., Montague M.A., Navas L., RA Newlon C.S., Olson M.V., Pallier C., Panzeri L., Pearson B.M., Perea J., Pilipsen P., Pierard A., Planta R.J., Plevani P., RA Sanz E., Schaeff-Gestenschlaeger I., Scherens B., Schweitzer B., Ra Shu Y., Skala J., Slonimski P.P., Sor F., Soustelle C., Thierry A., RA Van Vilet-Reddik J.C., Volckaert G., Vreken P., Warmington J.R., Ph. Von Wetter I., Marmington J.R., Won Wettstein D., Wicksteed B.L., Wilson C., Wurst H., Xu G., Thierry A., Thierry A., Steiner S., Schweitzer B., 
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Gromadka R.;
Gromadka R.;
between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             syndrome protein Lasi7p interacts with Mol. Biol. Cell 10:3521-3538(1999).
                                                                                                                                                                                                                                                                                                                                        Madania A., Dumoulin P., Grava S., Kitan
Soulard A., Moreau V., Winsor B.;
"The Saccharomyces cerevisiae homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dewar H., Warren D.T., Gardiner F.C., Gourlay C.G., Richardson M.R., Andrews P.D., Ayscough K.R., "Novel proteins linking the actin cytoskeleton to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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Oliver S.G., van
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MEDLINE=99443803; PubMe
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Nature 357:38-46(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22287476; PubMed=12388763;
                                                                                                                                                            SIMILARITY: TO S.POMBE SPBC31F10.07.
                                                                                                                                                                                                   SUBCELLULAR
                                                                                                                                                                                                                   FUNCTION: Bssential for the organization cytoskeleton, fluid phase endocytosis and together with YSCB4.
SUBUNIT: Interacts with SLA1 and LAS17.
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lin P., Grava S.,
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   RA Kunst F. Ogsaswara N., Moszer I., Albertini A.M., Alloni G., RRA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Ra Borriss R., Boursier L., Parans A., Barum M., Brignell S.C., Bron S., RA Borriss R., Boursier L., Parans A., Barum M., Brignell S.C., Bron S., RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Bamerson P.T., Ra Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Guiseppi G., Guy B.J., Kasahara Y., Klaerr-Blanchard M., Klein C., Robingstein G., Krogh S., Kumano M., Klein C., Robingstein G., Krogh S., Kumano M., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Lee S.M., Mellado R.P., Mizuno M., Moestl D., Nakai S., Naback M., RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Naback M., RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Ra Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sanlan E., Schleich S., Schroeter R., Scoffone F., Scanlan E., Schroeter R., Scoffone F., RA Scignichi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B., Rakuchi M., Tanakoshi A., Tanaka T., Takahashi H., Takemaru K., RA Viari A., Wambutt R., Wamanoto H., Vamane K., Yasumoto K., Yata K., Watara P., Wight A., Yamanoto H., Yamane K., Yasumoto K., Yata K.,
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Freymond P.-P., Karamata D.;
Freymond P.-P., Karamata D.;
Sequencing and analysis of two gga genes associated with the "Sequencing and analysis of two gga genes associated with the synthesis of the minor teichoic acid of Bacillus subbtilis 16:
Synthesis of the minor teichoic acid of Bacillus subbtilis 16:
Synthesis of the EMBL/GenBank/DDBJ databases.
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PIR; S74282; S74282.
GermOnline; 138870; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minor teichoic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ); S0000539; LSB5.
GC:0005938; C:cell cortex; IDA.
GC:0007015; P:actin filament organization;
GC:0006897; P:endocytosis; IMP.
GC:0006897; P:endocytosis; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR BSU35680.
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7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 32, Created)
(Rel. 32, Last sequence up
(Rel. 42, Last annotation
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    Last annotation update)
    biosynthesis protein ggaB

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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35772B575D40BEB2 CRC64;
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Yata K.,
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RESULT 4
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Best Local S
Matches
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Cell wall;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the swiss institute. There are to the European Bioinformatics Institute. There are to use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement greement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                             VATE CITLI STANDARD; PRT; 230 AA. 095WE7; CF-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last amotation update) Vacuolar ATP synthase subunit E (EC 3.6.3.14) (Vacuolar proton pump E subunit) (CLVE-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SubtiList; BG11192; ggaB.
InterPro; IPR001173; Glyco_transf.
InterPro; IPR007554; Glyphos_transf.
Pfam; PF00535; Glycos_transf2; 1.
Pfam; PF04444; glyphos_transf; 1.
Teichoic_acid_biosynthesis; Transferase;
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-!- FUNCTION: Involved i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U13979; AAA73513.1; -.
EMBL; Z99122; CAB15585.1; -.
PIR; E69631; E69631.
                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
eurosids II; Sapindales; Rutac
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"The comple
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                                                                                                                                                                                                                                                                         Citrus limon
                                                                                                                                                                                                                     NCBI_TaxID=2708;
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                                                                                                                                                Reuveni M., Sadka A.;
"Isolation of vacuolar
Citrus limon.";
                                                                                                                                                                                    rissue=Fruit;
                                                                                                                                                                                                 SEQUENCE FROM
SUBUNIT: V-ATPase is a peripheral catalytic V an integral membrane V c' and d).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Inv
                                                          in eukaryotic cells.
CATALYTIC ACTIVITY:
H(+)(Out)
                                                                                            ) Plant Gene Register PGR00-005.
FUNCTION: Subunit of the peripheral VI complex of vacuolar ATPase essential for assembly or catalytic function. V-ATPase is responsible for acidifying a variety of intracellular compartments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the glycosyltransferase family 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equires a license agreement (Somail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     900 AA;
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107154 MW;
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Vi
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ce of the
                        proton p
                                    heteromultimeric enzyme composed of complex (components A to H) attached
                                                                         + H(2)0 +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FA66495488C2C62F
                                                                                                                                                            subunit E
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Gram-positive
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terium Bacillus
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                                                                                               Pfam; PF019
Hydrolase;
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The model by non-profit institutions as not removed. entities requires a license agreement (See least)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosic eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Vacuolar ATP synthase subunit E (EC 3.6.3.14)
(Vacuolar proton pump E subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9MB46;
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Pfam; PF01991; vATP-synt_E; 1.
Hydrolase; ATP synthesis; Hydrogen ion transport.
SEQUENCE 230 AA; 26343 MW; 091360AEA11DE068 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
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                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      EMBL; AB037106; BAA89661.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBDINIT: V-ATPase is an heteromultimeric peripheral catalytic V1 complex (componer an integral membrane V0 proton pore complex ('' and d) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the V-ATPase E subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
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                                                                                                                                                      PF01991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SIKRDHNDYSK 11
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  Similarity 6; Conserv
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                                                                                                                                                                         IPR002842; ATPsynt
                                                                                                       230
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  Conservative
                                                                                                 vATP-synt_E; 1.
synthesis; Hydrogen
AA; 26285 MW; AA13
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                       54.5%;
Score 41; DB;
Pred. No. 4.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complex (components A to H) attached t proton pore complex (components: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB Pred. No. 4.5; 2; Mismatches
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                                                                                                       AA1361E787C68DDE CRC64;
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                                                                                                                                 transport
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                       DB 1;
4.5;
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                                                                                                                                                                                                                                                                                                                                                                                          EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compartments
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                                                                                                                                                                                                                                                                                                                                                                                             a collaboration - MBL outstation
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                                                                     Query Match
Best Local :
                                                       Matches
                                                                                                                                                                   EMBI; AB063521; BAC24357.1; ...
HANAR; MF 00208; -; 1.
InterPro; IPR000713; Mux_ligase.
InterPro; IPR004101; Mux_ligase_C.
InterPro; IPR005761; MuxE.
Pfam; PF01225; Mux_ligase_C; 1.
Pfam; PF02975; Mux_ligase_C; 1.
TIGRPAMS; TIGR01085; muxE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIGBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
(EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase).
                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flies, Wigglesworthia glossin
Nat. Genet. 32:402-407(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=22297718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wigglesworthia glossinidia brevipalpis.
                                                                                                                                       TIGRFAMs; TIGRO1085; murE; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Akman L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MURE OR WIGBR2110

    -!- FUNCTION: Cell wall formation. Diaminopimelic acid adding enzyme

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the
                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 heptanedioate.
PATHWAY: Peptidoglycan biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic (P
                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the murCDEF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamate + meso-2,6-diaminoheptanedioate = ADP + N-acetylmuramoyl-L-alanyl-D-gamma-glutamyl-meso-2,
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 208
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                                                      Similarity 7; Conserv.
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 NLSODHIDYHKNMM 221
                           SIKRDHNDYSKNPM
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(Rel. 42,
(Rel. 42,
                                                                                                               496 AA;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                               124
57220 MW;
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                                                                      52.6%;
50.0%;
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                                                       Score 41; DB Pred. No. 10; 3; Mismatches
                                                                                                                               ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                 AE624DA57ADDAC1B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496
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                                                                   DB
10;
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                                                                                     Length 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shiba T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphate + UDP-,6-diamino-
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                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
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                                                                                                                                                                                                                                                                                                                                   commercia.
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RESULT 7
P44\_PANTR
ID P44\_PANTR
AC P27473;

STANDARD;

PRT;

444

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RESULT
SELB_ME
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Best Local
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Q57918;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                       LT 8
_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Honda Y., Kondo J., Maeda T., Yoshiyama Shikata T., Ono Y.;
"Isolation and purification of a non-A, microtubular aggregates protein.";
J. Gen. Virol. 71:1999-2004(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992
01-AUG-1992
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takahashi K., Kitamura N., Shibui T., Ka
Yoshiyama Y., Maeda T., Kondo J., Honda
Shimizu Y.K., Teranishi Y., Nakanishi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequencing and expression in Escheric non-A, non-B hepatitis-associated microtubular J. Gen. Virol. 71:2005-2011(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-A non-B
                                                                                                                                   Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                            Methanococcus jannaschii.
                                                                                                                                                                                                                                            01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90034; BAA14082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91011345; PubMed=2170569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91011346; PubMed=2170570;
                                                               SEQUENCE FROM N.A.
                                                                                                        NCBI_TaxID=2190;
                                                                                                                                                                                      Out-NOV-1997 (Rel. 35, Created)
11-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-lenocysteine-specific elongation factor (Section Rel. 40, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDUCTION: During infection or hepatitis delta virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jen. Virol. 71:1999-2004(1990).
FUNCTION: This protein aggregates
                                                                                                                                                                                                                                                                                                                                                                                                                                                286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microtubule.
Microtubule.
14 aA; 50471 MW;
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(Rel. 23, Last sequence update)
(Rel. 42, Last annotation update)
hepatitis-associated microtubular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Pred. No. 21;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             799CC855018CFA71 CRC64;
    Zhou
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                                                                                                                                                                                                                                                                                                                                     469
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da Y., Yamada
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                                                                                                                                                                                                                          (SelB translation factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
    Fleischmann
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    R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of cDNA for a es protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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RESULT 9
SMC4\_YEAST
ID SMC4\_YEAST
AC Q12267;
DT 10-OCT-2003
DT 10-OCT-2003
DT 10-OCT-2003
DE STRUCTURAL T
GN SMC4 OR YLRG
OS Saccharomyce

10-OCT-2003 10-OCT-2003 10-OCT-2003

(Rel. 42, Created)
(Rel. 42, Last sequence up
(Rel. 42, Last annotation

STANDARD;

1418

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Structural maintenance of chromosome SMC4 OR YLR086W OR L9449.5. Saccharomyces cerevisiae (Baker's years)

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                                                                   Query Match
Best Local S
Matches 8
                                                                                                                                      InterPro; IPR000795; EF GTPbind.
InterPro; IPR004161; EFTU D2.
InterPro; IPR004225; Small GTP.
InterPro; IPR005225; Small GTP.
InterPro; IPR00525; Small GTP.
InterPro; IPR004535; TEF SelB.
InterPro; IPR004055; TEF SelB.
InterPro; IPR009000; Translat_factor.
Pfam; PF00104; GTP EFTU D2; 1.
Pfam; PF00315; EFOUNDATNFCT.
TIGRPAMS; TIGR00475; selB; 1.
PROSITE; PR00315; small GTP; I.
PROSITE; PS00301; EFACTOR GTP; FALSE NEG.
PROSITE; PS00301; EFACTOR GTP; FALSE NEG.
PROSITE; PS00301; EFACTOR GTP; GTP (BY SIMILARITY).
PSIND 16 23 GTP (BY SIMILARITY).
NP_BIND 123 126 GTP (BY SIMILARITY).
SEQUENCE 469 AA; 51849 MW; F3C1863CAAF04A92 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Biol. 299:351-358 (2000).

J. FUNCTION: Translation factor necessary for the incorporatelement of the incorporate selenocysteine into proteins. It probably replaces EF-Tu selenocysteine directed by the UGA codon. St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutton G.G., Blake J.A., FitzGerald I.M., Clayton R.A., Gocayne J.D. Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.I., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D. Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; G64361; G64361.
HSSP; P07157; 1AIP.
TIGR; MJ0495; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentities requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rother M., Wilting R., Commans S., Boeck A.; "Identification and characterisation of the selenocysteine-specific translation factor SelB from the archaeon Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20318769; PubMed=10860743; Rother M., Wilting R., Commans S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67499; AAB98485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )annasch:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP and GDP.
SUBCELLULAR LOCATION: Cytoplasmic.
SUMILARITY: Belongs to the GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SelB subfamily.
182
                               N
                                                                   8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273:1058-1073(1996).
IKRDINSYLKMPI 194
                               IKRDHNDYSKNPM 14
                                                                      Conservative
                                                                                       50.0%;
                                                                    Score 39; DB Pred. No. 23; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                    Complete proteome.
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                                                                                                          <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elongation
                                                                                                          Length 469;
                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       incorporation aces EF-Tu for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon. SELB binds
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RC STRAINS-S286C / AB972;

RX MEDLINE-S286C / AB972;

RX MEDLINE-S7313267; pubMed=9169871;

RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,

RA Johnston M., Hillier L., Riles L., Dubois E., Duesterhoeft A.,

RA Henes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,

RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,

RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

RA Houis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

RA Mueller-Auer S., Nentwich U., Obermaier B., Rieger M., Rinke M., Rose M.,

RA Mueller-Auer S., Scherens B., Scholler P., Schwarz S.,

RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

RA Mether H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

RA Mether H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

RA Mether H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLINE=20273907; PubMed=10811823;

WEDLINE=20273907; PubMed=10811823;

WEDLINE=20273907; PubMed=10811823;

"The condensin complex governs chromosome condensation and mitotic running from the complex governs chromosome condensation and mitotic running from transmission of rDNA.";

1. Cell Biol. 149:811-824(2000).

1. Cemponent of the condensin complex is found in the complex is associated with the component of the condensin associated with the chromosome condensin on associated with the chromosome condensin on associated with the chromosome of the condensation. Dissociation from the component of the condensation. Dissociation from the component of the condensation.
   SGD; S0004076; SMC4.
GO; GO:000799; C:nuclear condensin complex; IPI.
GO; GO:0007076; P:mitotic chromosome condensation; IMP.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_C.
InterPro; IPR003395; SMC_N.
Pfam; PF02483; SMC_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-siorsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                EMBL; Z73258; CAA97646.1; -.
EMBL; Z73259; CAA97648.1; -.
EMBL; U53880; AAB67590.1; -.
PIR; S64918; S64918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.
STRAIN=S288c / A
                                                                                                                                                                                                                                                          GermOnline; 142148; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICIATION IN A CONDENSIN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosomes is observed in late telophase.

DOMAIN: The flexible hinge domain, which separates the large intramolecular coiled coil regions, allows the heterodimerization with SMC2, forming a V-shaped heterodimer (By similarity).

SIMILARITY: Belongs to the SMC family. SMC4 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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Best Local S
Matches 6
R EMBL; Z34098; CAA83991.1; -.

R EMBL; Z44944; CAA839516.1; -.

R PIR; S50708; S50708.

R Germonline; 141831; -.

R GG; GO:005353; F:fructose transporter activity; IGI.

RG; GO:0005354; F:galactose transporter activity; IGI.

RG; GO:0005355; F:glucose transporter activity; IGI.

RG; GO:0005355; F:glucose transporter activity; IGI.

RG; GO:000545; P:hexose transporter activity; IGI.

RG; GO:0008645; P:hexose transporter.

RINterPro; IPR007114; MFS.

RR InterPro; IPR005828; Sub_transporter.

InterPro; IPR005829; Sug_transporter.

InterPro; IPR00363; Sugar_transporter.

RR InterPro; IPR00363; Sugar_transporter.

RR PINTS; PR00171; SUGAR_TRANSPORT_1; 1.

RR PROSITE; PS00216; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P40885;
01-FEB-1995
01-FEB-1995
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NP BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
HXT9_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hexose transporter HXT9.

HXT9 OR YULL19W OR J0222 OR HRC567.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast 10:1657-1662(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of a 40.2 telomere of yeast chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95242842; PubMed=7725802;
Vandenbol M., Durand P., Bolle P.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: PROBABLE GLUCOSE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hilger F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     condensation;
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6; Conserve
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674
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COILED COIL (POTENTIAL).
FLEXIBLE HINGE.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
B MM; F0B6B72FE8BFD374 CRC64
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Pred. No. 77;
2; Mismatches
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01-APR-1993
01-APR-1993
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
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CARBOHYD
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TRANSMEM
                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mitochondrial processing peptidase alpha subunit, mitochondrial
precursor (EC 3.4.24.64) (Alpha-MPP) (Ubiquinol-cytochrome C re
subunit II) (EC 1.10.2.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                               EMBO
                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embry Spermatophyta; Magnoliophyta; eudicotyledons; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                          Braun H.P.,
                                                                                                                                 STRAIN=cv. Desiree; TISSUE=Green
MEDLINE=92371428; PubMed=1324169;
                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                     NCBI_TaxID=4113;
                                                                                                                                                                                                            Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                      "The general mitochondrial processing peptidase from potato integral part of cytochrome c reductase of the respiratory
mitochondrial protein precursors (By similarity).

FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), IS PART OF THE MITOCHONDRIAL RESPIRATORY CHAIN.

MEDIATE FORMATION OF THE COMPLEX BETWEEN CYTOCHROMES C AND CATALYTIC ACTIVITY: Release of N-terminal transit peptides f precursor proteins imported into the mitochondrion, typicall Arg in position p2.

CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
                                                                                     FUNCTION: Cleaves presequences (transit peptides)
                                                                                                                                                                                                                                                                                               SOLTU
                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                              1 SIKRDHNDYSKNPM 14
                                                                                                                                                                                                                                                                                                                                                                                . Similarity
8; Conserv
                                                                                               11:3219-3227(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                    227
567
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                           AND SEQUENCE
TISSUE=Green
                                                                                                                                                                                                                                                                                                                                                                                          49.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        3
                                                                                                                          Kruft V.,
                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
2CF4C8617D9B2701 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transport; Transport; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL) 8 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL) 4 (POTENTIAL).
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3 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
CYTODE A COLOR
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11 (POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
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9 (POTENTIA:
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                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                           OF 270-280 AND 400-419 leaf;
                                                                                                                                                                                                                                                                                                                                                                                            No. 34;
                                                                                                                          Schmitz U.K.;
                                                                                                                                                                                                                                                                                                504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR (POTENTIAL)
                                                                                                                                                                                                   Embryophyta; Tracheophyta,
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                                                                                                                                                                                          eudicots; asterids;
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Pfam; PF005193; Peptidase M16 C; 1.

PROSITE; PS00143; INSTLINASE; 1.

PHOTOR METALOROCOMERS; Mitochondrion; Transit peptydrolase, Metalloprotease, Mitochondrion; Transit peptydrolase, Mitochondrion; Mitochondrion; Transit peptydrolase, Mitochondrion; Transit peptydrolase, Mitochondrion; Transit peptydrolase, Mitochondrion; Mitochon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                        Mahalingam R., Seilhamer J.J., Fritchard A.E., Cummings D.J.;
Mahalingam R., Seilhamer J.J., Fritchard A.E., Cummings D.J.;
Midentification of Paramecium mitochondrial proteins using antibodies
raised against fused mitochondrial gene products.";
Gene 49:129-138(1986).

-I- FUNCTION: Cytochrome c oxidase is the component of the respiratory
chain that catalyzes the reduction of oxygen to water. Subunits 1-
3 form the functional core of the enzyme complex. Subunit 2
transfers the electrons from cytochrome c via its binuclear copper
A center to the bimetallic center of the catalytic subunit 1.

-I- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988 (Rel.
01-AUG-1988 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARPR
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                                                                                            +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Paramecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P08748;
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TRANSIT
1 ? MITOCHONDRIAL PROCESSING PEPTIDASE
CHAIN ? 504 ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001431;
InterPro; IPR007863;
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                                            inner membrane.
-!- SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87191992; PubMed=3032745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paramecium primaurelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COX2_PARPR
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SUBCELIUIAR LOCATION: Mitochondrial inner mebrane.
SIMILARITY: Belongs to peptidase family Mi6.
CAUTION: Does not seem to have a protease activity as it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zinc-binding site.
                                                                                                 SUBCELLULAR
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                                                                                                 Copper A.
AR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08, Created,
08, Last sequence update)
41, Last annotation update)
41, Description (EC 1.9.3.
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50.0%;
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Pred. No.
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                                               cytochrome c oxidase subunit 2 family.
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                                                                                                    membrane protein.
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InterPro; IPR008972; Cyt_c_ox_2.
InterPro; IPR002429; Cyt_c_ox_2.
Pfam; PF00116; COX2; 1.
PRINTS; PR01166; CYCOXIDASEII.
ProDom; PD000131; Copper CuA; 1.
PROSITE; PS00078; COX2; FALSE NEG.
Oxidoreductase; Copper; Mitochondrion; Tr
Electron transport; Respiratory chain.
Electron transport; Respiratory chain.
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P81942;
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the Euro
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                                                                           structural properties.";

Biochem. J. 322:679-680(1997).

-i-FUNCTION: Conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles.

-i- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97218132; PubMed=9065793;
Sacchetta P., Petruzzelli R., Melino S., Bucciarelli Amicarelli F., Miranda M., Di Ilio C.;
"Amphibian embryo glutathione transferase: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bufo bufo (European toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003
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                                                                                                                                                Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
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HSSP; P19157; 1BAY.
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                                                                                                                                                                                             InterPro; IPR004046; GST_Cterm.
InterPro; IPR004045; GST_Nterm.
InterPro; IPR003082; GST_pi.
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European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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Similarity 6; Conser
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(Rel. 41, Last seq
(Rel. 41, Last ann
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130
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  Conservative
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130
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                    47.4%;
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Last annotation update)
rase P 1 (EC 2.5.1.18) (
; Score 37; DB;
; Pred. No. 21;
3; Mismatches
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Pred. No.
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1; Mismatches
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COPPER A (PROBABLE).
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; 910481DF1A455A76 CRC64;
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                         DB 1;
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Bufonidae; Bufo
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RESULT 14
OXA2 STARES
ID OXA2 STARES
AC Q8CMK8
AC Q8CMK8
DT 15-MAR
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FT TRANSS
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Matches 6
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OXAA2 OR SE1889.

Staphylocor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; Year Z., Zhao B., Danchin A., Wen Y.-M.; "Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228)."; Mol. Microbiol. 49:1577-1593(2003).
                                                                                                                                                                                             TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                     HAMAP; MF_01811; -; 1.
InterPro; IPR001708; 60kDa innermeb.
InterPro; IPR000437; Prok Tipoprot_S.
Pfam; PF02096; 60KD IMP; 1.
PRINTS; PR00701; 60KDINNERMP.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8CMK8;
                                                                                                                     SEQUENCE
                                                                                                                                   CIAIT
CIAIT
                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE016749; AA005288.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
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                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the OXA1/oxaA family. Subfamily
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                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                       Transmembrane;
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SUBCELLULAR LOCATION: Inte
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267
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EREHNPYSK
                            KRDHNDYSK 11
                                                                                                                   290 AA;
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                                                           Conservative
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                                                                                                                                                                                                                                                                        Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: Integral membrane
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154
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224
251
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                                                                      47.4%;
66.7%;
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                                                                                                                                                                                                                                                                                        LIPOPROTEIN;
                                                                                                                     MW;
                                                                                                                                                                                                                                                       Signal; Par
POTENTIAL.
                                                         Score 37; DB
Pred. No. 30;
2; Mismatches
                                                           2
                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                   N-palmitoyl cysteine (Potential) S-diacylglycerol cysteine (Poten ; 913063238F04D09E CRC64;
                                                                                                                                                                                                                                              MEMBRANE PROTEIN OXAA
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                                                                    30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions as its content is in
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RESULT 15
VG06\_BPML5
ID VG06\_BPML5

STANDARD;

PRT;

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Search completed: March 22, 2004, 06:52:53 Job time : 2.53696 secs
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                                                                                                          δ
                                                                                                                                                                                                                         Query Match 47.4
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                     EMBL; Z18946; CAA79385.1; -. 
PIR; S30954; S30954. 
INIT MET 0 0 
SEQUENCE 312 AA; 33890 NW;
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-11.

MEDILINE=93211282; PubMed=8459766;

Hatfull G.F., Sazkis G.J.;

"DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics,";

Mol. Microbiol. 7:395-405(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q05278;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacteriophage L5.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
L5-like viruses.
NCBI_TaxID=31757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minor tail protein GP6.
                                                                          72 DYNDVSENP 80
                                                                                                 5 DHNDYSKNP 13
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312 AA; 33890 MW; 0D392580248349B3 CRC64;
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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
  protein search, using sw model
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Match
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1: sp_archea:*
2: sp_bacteria:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9TKN6
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                             Q9s489 prochloroco
Q7v2b7 prochloroco
Q8ikn6 plasmodium
Q7ugm6 rhodopirell
Q91yv4 mus musculu
Q8c9f1 mus musculu
Q8c9f7 mus musculu
                                                                                                            Q9u6r7 dermatophag
Q8i154 plasmodium
Q9u6v8 drosophila
Q9u6v8 drosophila
Q9h8k7 homo sapien
Q8i3v2 plasmodium
Q08461 drosophila
            Q9ury8
Q9n4x7
                                                                                                                                                                                            Description
 Q8dak4 vibrio vuln
           schizosacch
caenorhabdi
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	Q91F03	12	342	0	39	45
$^{\circ}$	Q9C125	W	284	0	39	44
270 staphyl	Q54270	N	273	50.0	39	43
	Q7T5N9	12	206	0	39	42
88c16 pseudomona	Q88C16	16	156	0	39	41
	Q8EEK2	16	112	0	39	40
O25761 helicobacte	025761	16	759	0	9	u 9
Q8i6q2 anopheles s	Q816Q2	υī	575	0	39.5	38
Q8i3h5 plasmodium	Q813H5	ഗ	548		9	37
Q7xes0 oryza sativ	Q7XES0	10	296		9	ა 6
plasmodium	QBILL7	υī	1621	۳	40	35 5
Q95p23 aplysia cal	Q95P23	υı	837	۲	40	34
Q9s222 streptomyce	Q9S222		548	:-	40	ω ω
Q7ykk5 utricularia	Q7YKK5		505		40	32
Q7w0d5 bordetella	Q7W0DS		470		40	31
Q7w1q1 bordetella	Q7W1Q1		470	<u></u>	40	30
bor	Q7WQM7		470		40	29
Q8n597 homo sapien	Q8N597		445		40	28
bor	051621		383		40	27
	Q25361		228		40	26
strep	Q9ZEP5		202	۳	40	25
Q8tsh2 methanosarc	Q8TSH2		180		40	24
Q8ibh8 plasmodium	Q8IBH8	ហ	1923		41	23
2 oryza sat	Q7XS42	10	1645	'n	41	22
Q86ks1 dictyosteli	Q86KS1	υı	920	'n	41	21
rickettsi	Q92H92	16	906	٥	41	20
	Q7X081	N	906	٢	41	19
Q8ihs7 plasmodium	Q8IHS7	ហ	899	Ņ	41	18
Q8iky2 plasmodium	Q8IKY2	ហ	748	Ņ	41	17

### ALIGNMENTS

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Q8IL54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9U6V8;
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GO; GO:0003824; F:catalytic activity;
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila willistoni (Fruit
Eukaryota; Metazoa; Arthropod
Neoptera; Endopterygota; Dipt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 419:498-511(2002).
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NCBI_TaxID=36329;
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                               retrotransposon.";

Proc. Natl. Acad. Sci. U.S.A. 96:126:

EMBL; AF175766; AAF06354.1; -.

FlyBase; FBgn0044137; Dwil\copia\GIP
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Royal Palm Park; TRANSPOSON
MEDLINE=20006284; PubMed=10535972;
                                                                                                                                                                        Jordan I.K., Matyunina L.
"Evidence for the recent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                 _TaxID=7260;
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKOHNEYYTNP
                                                                                                                                                                                                                                                                                                                                                                                                             ; Metazoa; Arthropoda;
Endopterygota; Diptera
ea; Drosophilidae; Dros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 protein.
569 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence up
(TrEMBLrel. 25, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13,
13,
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                                                                                                                                                                                                                                                                           TRANSPOSON=copia;
                                                                                                                                                                                                                                                                                                                                                                                                             ropoda; Hexapoda; Insecta; Pterygota;
Diptera; Brachycera; Muscomorpha;
ae; Drosophila.
                                                                                                                                                                        .V., McDonald J.F.; horizontal transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation updat
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Pred. No. 18;
2; Mismatches
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                                                                                                     96:12621-12625(1999).
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                                                                                                                                                                            terminal
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RESULT CONTROL OF CONT
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Best Local S
Matches 9
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Best Local
                                                                                                                  Hypothetical protein.

PFE0780W.

Plasmodium falciparum (
Bukaryota, Alveolata, A
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITSSUE=Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Nihomiya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ13490.
Homo sapiens (Human)
                   SEQUENCE FROM N.A.
Devlin K., Baker S.,
Hall N., Bowman S., C
Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9H8K7;
Q9H8K7;
                                     Devlin K.,
                                                                                                                                                                                                                                  01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                          Q8I3V2;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 445 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0006810; P:transport; IEA.
InterPro; IPR003439; ABC transporter.
PROSTIE; PS00211; ABC TRANSPORTER_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AKC23552; BAB14609.1; -...
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                      Q8I3V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
7; Conserv
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239 AA;
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                                                                                                                                                                                                                                (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                          (TrEMBLrel.
                 S., Davies P., Mungal K., Berriman M., S., Churcher C., Quail M., Barrell B.; 002) to the EMBL/GenBank/DDBJ databases
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27400 MW;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49250 MW;
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                                                                                                                                               (isolate 3D7)
Apicomplexa;
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Pred. No.
                                                                                                                                                                                                                                                                          Created)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D08E8B3124EE5189 CRC64;
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                                                                                                                                                                     3D7)
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                                                                                                                                          Haemosporida;
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21;
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                                                                                                                                                 Plasmodium
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RESULT
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A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Mights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
RA Rajandream M.A., S., Smith R., Squares R., Squares S., Stevens K.,
RA Raylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G., 2-and 12 ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 7
Query Match
Best Local S
Matches 9
                                                                                                                                               Pfam; PF00665; rve; 1.

Pfam; PF00098; zf-CCHC; 1.

PRINTS; PR00939; C2HCZNFINGER.

SMART; SM00343; ZnF CCHC; 1.

PROSITE; PS50158; ZF CCHC; 1.
                                                                                                                                                                                                                                                                           EMBL; D10880; BAA01703.1; -.

MEROPS; A11.001; -.

FlyBase; FBgn0044190; Dsim\copia\GIP.

GO; GO:0003577; F:DNA binding; IEA.

GO; GO:0005310; P:DNA recombination; IEA.

InterPro; IPR001584; Rve.

InterPro; IPR001578; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1)
SEQUENCE FROM N.A.
MEDLINE=93013034; PubMed=1383092;
MEDLINE=93013034; PubMed=1383092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPIA\GIP.
Drosophila simulans (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 419:527-531(2002).
EMBL; AL929352; CAD51520.1; -.
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                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        like particle.";
Gene 120:191-196(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshioka k., Kanda H.,
Sakaki Y., Shiba T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003
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MEDLINE=22255708;
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Similarity
9; Conserv
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                                                                                                         1409 AA;
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1250 AA;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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77.8%;
                        57.7%;
69.2%;
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                                                                                                      162899 MW;
Score 45; DB Pred. No. 72; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB pred. No. 63; 1; Mismatches
                                                                                                      MAJOR COPIA VIRUS-LIKE PARTICLES W; 403A9FFF66A21903 CRC64;
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                                                Length 1409
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Query Match
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Matches
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Best Local
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Q9S489;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Prochlorococus sp. Strain PCC 9511.";

J. Bacteriol. 183:915-920(2001).

Check, AR158628; AAD45693.1;

Check, AR158628; AAD45693.1;

Check, AR158628; AAD45693.1;

Check, AR158628; AAD45693.1;
                                                                               MEDIINE=22825698; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb B.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects on
niche differentiation.";
Nature 424:1042-1047(2003).
                                                                                                                                                                                                                              Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4). Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae; Prochlorococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF158628; AAD45693.1; -.
InterPro; IPR001173; Glyco_trans_2.
Pfam; PF00535; Glycos_transf_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21142517; PubMed=11208789;
Holtzendorff J., Partensky F., Jacquet
Garzzarek L., Mary I., Vaulot D., Hess
"Diel Expression of Cell Cycle-Related
                                                Hypothetical
SEQUENCE 22
                                                                                                                                                                                                                                                                                                                Q7V2B7;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                          Q7V2B7
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                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                        EMBL; BX572091; CAE19022.1;
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 Similarity 9; Conser
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75.0%;
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25,
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                                                          lete
Score 44; DB; Pred. No. 15; 0; Mismatches
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Pred No. 15;
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5E1EB4F18559F019 CRC64;
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Eukaryota; Alveolata;
NCBI_TaxID=36329;
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Rhodopirellula baltica.
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01-OCT-2003 (TrEMBLrel.
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01-OCT-2003
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MEDLINE=22255705; PubMed=12368864;
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                                                                                                                                                                                                                         MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot Gloeckner Gode D., Beck A., Borzym K., Heitmann K., Rabb Schlesner H., Amann R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
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                                                                                            "Complete genome sequence of t
strain.";
Proc. Natl. Acad. Sci. U.S.A.
EMBL; BX294141; CAD78303.1; -.
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                                                                     Complete
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                                       proteome.
576 AA;
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01-OCT-2003
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01-MAR-2003
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PROSITE; PS50082; WD_REPEATS_REGION; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

Hypothetical protein; Repeat; WD repeat.

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SEQUENCE 601 AA; 68243 MW; F0470922F
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4921524P20RIK.
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
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Mammalia; Eutheria;
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4921524P20RIK.
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                                                                             the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                     EMBL; AK042231; BAC31200.1; -. MGD; MGI:1915509; 4921524P20Rik.
                                                                                                                                                              The FANTOM Consortium,
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Pro; IPR001680; PF00400; WD40;
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l protein (Fragment).
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Rodentia;
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(Fragment).
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Pred. No.
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Sciurognathi; Muridae;
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PROSITE; PS50294; WD_REPEATS_REGION; 1.
Hypothetical protein.
NON_TER 751 751
NON_TER 751 AA; 84910 MW; B78CA8DACE7E6157 CRC64;
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PROSITE: PS50294; WD_REPEATS_REGION;
Repeat; WD repeat.
SEQUENCE 777 AA; 87810 MW; 2B0162
                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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EMBL, BC034101; AAH34101.1; -.
MGDJ, MGI.1915509; 4921524P20Rik.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similar to KIAA1374
4921524P20RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8K057
                             Hunt C., Aves S., McDougall Submitted (NOV-1999) to the EMBL; AL132779; CAB60015.1; PIR; T39116.
                                                                                                                                                            STRAIN=972h-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Õ9URY8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9URY8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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(TrEMBLrel. 13, Last seq
(TrEMBLrel. 24, Last ann
lfate permease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Rodentia;
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63.6%;
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Last annotation updat
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Pred. No. 1.2e
3; Mismatches
                                                                                             R.C., Rajandream M.A., Barre EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No.
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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chi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
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GeneDB\_SPombe;

Search completed: March Job time: 5.81712 secs

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RESULT 15
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Best Local
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GO; GO:0008271; F:sulfate porter activity; IE
GO; GO:0008272; P:sulfate transport; IEA.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PF001740; STAS; 1.
Pfam; PF001740; SULfate_transp; 1.
IIGRPAMs; TIGR00815; Sulph_transp; 1.
PROSITE; PS50801; STAS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                             Bradshaw H., Graves T.,
"The sequence of C. elec
Submitted (MAR-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical Y45G12C.1.
                                                                                                                                                                                WormPep; Y45G12C.1; C
Hypothetical protein.
SEQUENCE 378 AA; 4
                                                                                                                                                                                                                          Submitted (JUL-2001) to the EMBL; AC006769; AAF60579.1; WormPep; Y45G12C.1; CE21936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology. The C Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            None;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                    Waterston R.;
                                                                                                                                                                                                                                                                                                   Direct Submission.";
362
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                                                                                       Similarity 7; Conserva
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                                            RDHNDYSKNP 13
RDHNHYFMNP 371
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(TrEMBLrel.
                                                                                           Conservative
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                                                                                                                                                                                  44406 MW;
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                                                                                                              52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                           Fronick B.;
gans cosmid Y45G12C.";
the EMBL/GenBank/DDBJ
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25,
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Last sequence update)
Last annotation updat
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                                                                                       Score 41; DB
Pred. No. 86;
0; Mismatches
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Pred. No.
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
39.
39
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Match Length
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m2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
m2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
m2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
m2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
m2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
m2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
m2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
m2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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gm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
gm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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gm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
gm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
gm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
gm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-10-218-743-24
US-10-218-743-15
US-10-218-743-15
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US-10-218-743-3-8
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US-10-424-599-259092
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                                                                                                               Sequence 1, Appli
Sequence 24, Appl
Sequence 27, Appl
Sequence 15, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 35, Appl
Sequence 38, Appl
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Sequence
Sequence
      sequence 148, App
Sequence 48754, J
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                                      262038,
47229, A
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464, App
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US-10-218-743-1

## ALIGNMENTS

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TYPE: PRT
CRGANISM: Dermatophagoides farinae
US-10-218-743-1
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CURRENT FILING DATE: 2002-08-13
PRICR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1990-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR PPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                  Matches
                                                                                         Query Match
Best Local :
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
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14; Conservative 0
SIKRDHNDYSKNPM 14
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Pred. No. 1.2e-06;
); Mismatches 0;
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1990-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR PPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
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PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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NUMBER OF SEQ ID NOS:
SOPTWARE: PatentIn Ver
SEQ ID NO 21
LENGTH: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
                                                                                                                                            PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
                                                                                                                  PRIOR FILING DATE: 1998-04-17
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PELICANT: Weber, Eric R.
PELICANT: Weber, Eric R.
PELICANT: WOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITLE OF INVENTION: AND USES THEREOF
TLE REFERENCE: AL-2-C3
TLE REFERENCE: AL-2-C3
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Similarity 100.0%;
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o. US20030096779A1
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Pred. No.
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Sequence 18, Application US/10218743

Publication No. US20030096779A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: MCCall, Catherine A.
APPLICANT: Weber, Eric R.

ITILE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROT TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROT TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: AL-2-C3

CURRENT SILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: US/10/218,743

CURRENT FILING DATE: 1999-04-L5

PRIOR APPLICATION NUMBER: 00/098,909

PRIOR FILING DATE: 1998-09-02

PRIOR FILING DATE: 1998-09-02

PRIOR FILING DATE: 1998-09-03

PRIOR APPLICATION NUMBER: 60/098,565

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-04-17
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CURRENT FILING DATE: 2002-08-13
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERVATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
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PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/098,909
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PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
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PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
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Pred. No. 6.
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SEQ ID NO 18
LENCTH: 555
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SEQ ID NO 41
LENGTH: 490
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Best Local Similarity
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                                                                                                                                                                                                                                  Sequence 35, Application US/10218743 Publication No. US20030096779A1
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APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR PILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
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PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
                                                                  APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERNATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
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PRIOR APPLICATION NUMBER: 60/098,565
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CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 49
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ORGANISM: Dermatophagoides farinae
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RESULT 9 US-10-424-599-259092

Sequence 259092, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K

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APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
ITILE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR TILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08,565
PRIOR PILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR PILING DATE: 1998-04-17
PRIOR PILING DATE: 1998-04-17
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SEQ ID NO 35
LENGTH: 509
                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
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SEQ ID NO 38
LENGTH: 509
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
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PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
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                                                                                                                                                                                                     ORGANISM: Dermatophagoides farinae
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KRDHNNYSKNPM 33
                                            KRDHNDYSKNPM 14
                                                                                           Conservative
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91.7%;
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91.7%;
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Pred. No. 0.0098;
                                                                                      Score 65; DB 14; Pred. No. 0.0098; 1; Mismatches
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US-10-259-165-464; Sequence 464, Application US/10259165; Publication No. US20030135888A1
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US-10-424-599-259092
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CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 259092
LENGTH: 355
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentList.pl version
SEQ ID NO 134
LENGTH: 587
TYPE: PRT
ORGANISM: Oryza sativa
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Publication No. US20030135888A1
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Best Local
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IITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
IITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LICANT: Moughamer, Todd
LICANT: Provart, Nicholas
LICANT: Ricke, Darrell
LE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
E REFERENCE: 70030-NP
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6; Conserv
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Cooper, Bret
Glazebrook, Jane
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Chang, Hur-song
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Pred. No.
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentList.pl version 3.0.4 (C) 20
SEQ ID NO 464
LENGTH: 587
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US-10-424-599-262038
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US-10-259-165-464
                                                                                                                                             US-10-424-599-262038
                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Xovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 262038
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 262038, Application US/10424599
Publication No. US20040031072A1
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                                                                       Matches
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Best Local
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PPLICANT: Moughamer, Todd
PPLICANT: Provart, Nicholas
PPLICANT: Ricke, Darrell
ITLE OF INVENTION: GENES THAT ARE MODULATED
ILE REFERENCE: 70030-NP
                                                                                                                                                            FEATURE:
OTHER INFORMATION: Clone
                                                                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                                                                      TYPE: PRT
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25
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                                                                                      Similarity
                                   SIKRDHNDYSKNP 13
SKKRVHPDYGSNP 37
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Chang, Hur-song
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                                                                       Conservative
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                                                                                      51.3%;
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                                                                     Score 40; DB Pred. No. 18; 0; Mismatches
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                                                                                                           12;
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RESULT 13

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Sequence 148, Application US/09881752A
Patent No. US20020115078A1
GENERAL INFORMATION:
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Publication No. US20040029129A1
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Best Local
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               APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Encoding No. U
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
                                                                                                                    APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
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PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 2000-03-21
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CURRENT FILING DATE: 2003-02-20
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FILE REFERENCE: ELITRA.034A
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JRRENT APPLICATION NUMBER: US/09/881,752A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
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FILING DATE: 2000-11-27
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FILING DATE: 2000-10-23
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7; Conservation
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Yamamoto, Robert
Forsyth, R.
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Zyskind, Jud
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Malone, Cheryl
Haselbeck, Robert
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lio, Carlos
                                  Identification of Polynucleotides
Encoding No. US20020115078A1el Helicobacter Polypeptides in
Genome
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Pred. No. 1.3e+02;
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; ORGANISM: Bacteroides US-10-282-122A-48754
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US-10-282-122A-48754
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SEQ ID NO 148
LENGTH: 442
                                                                          SOFTWARE: PatentIn version SEQ ID NO 48754
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PRIOR FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR DATE: 2000-03-21
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PRIOR APPLICATION NUMBER: US 08/833,
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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Yamamoto, Robert
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78
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(c) 1993 - 2004 Compugen Ltd.
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Aau81523 Human Che Aay82948 MIS toxin	Abu43951 Protein e	Abu50622 Protein e	Abb60202 Drosophil	Abb67020 Drosophil	-	Abm70283 Photorhab	Abb63478 Drosophil	Protein				Abr53853 Protein s			Human	w	0	s. pn

# ALIGNMENTS

22-FEB-2000 AAY52510;

(first entry)

House dust mite allergen protein (map) A/B N-terminal fragment

AAY52510 standard; peptide; 14 AA.

Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation. 02-SEP-1998; 17-APR-1998; 13-MAY-1998; 16-APR-1999; 28-OCT-1999. Dermatophagoides farinae. Mccall CA, WO9954349-A2 (HESK-) HESKA CORP. Hunter SW, 98US-00062013. 98US-0085295P. 98US-0098909P. 99WO-US008524. Weber

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Claim 3; Page 69; 154pp; English.

WPI; 2000-052700/04.

Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWM nempt) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. The HMW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines,

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Query Match
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                                                                             Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the allergic response to a mite animal animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus
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                                   reducing hypersensitivity responses to mite allergens, and as vacci
against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                 The invention relates to an isolated mite allergenic protein of
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                                 Der HMW-map polypeptides
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Pred. No. 8.
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8.7e-07;
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13-MAY-1998;
02-SEP-1998;
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This sequence represents an N-terminal proteolytic fragment of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM nemap) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to
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                                                                                                                                                                                                              high molecular weight Dermatophagoides nucleic acid polypeptides to modify an animals' hypersensitivy to mite allergens.
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                                                                                                                                         Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a nongrotein susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a nanimal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the callergic response to a nati-Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
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Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page
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                                                                                           Sequence 33
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Pred. No. 2.4e-06;
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Pred. No.
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                                                                 This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-536, the mature form of PDerf98-556 (AAY5253). PDerf98-536 chas a molecular weight of 98 kD, comprising 536 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) composition. The HMM-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to 1g2 present in mite-allergic dog antisera. Mite allergenic proteins and compositions to motify an animal's hypersensitivity reaction to mite compositions to motify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, cespecially felines, canines, equines, humans, other pets, and work or composition to a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, can be used as vaccines to passively immunise animals as adainst that hypersensitivity, as positive controls in test kits and as tools to control to the proteins.
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02-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 125-127; 154pp; English.
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98US-0085295P.
98US-0098909P.
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RESULT 6
AAU96329
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                                                                                                                                                                                                                                                                                                                      Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a nongroup protein accoust epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal to an allergic response to a mite. The DNA and protein can be used in the categories of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a clisease. Antibodies that bind to Der HMW-map are useful for inhibiting chinding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 or represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated mite allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mccall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-2001; 2001WO-US028730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dermatophagoides farinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mite allergenic protein; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Der HMW-map; American house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Der HMW-map polypeptide #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2002
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                                                                                                                                                                                                                                                                                                 Sequence 536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA CORP
                             House dust mite
                                                        22-FEB-2000
                                                                                   AAY52523;
                                                                                                              AAY52523 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
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DB; ABK69575.
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                                                                                                                                                                                                                                          14;
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                                                                                                                                                                                                              1 SIKRDHNDYSKNPM 14
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                    SIKRDHNDYSKNPM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 125-127; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hunter
                                                                                                                                                                                                                                          Conservative
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                                                        (first entry
                             ê.
                             farinae)
                                                                                                                                                                                                                                                       100.0%;
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immunoglobulin E; hypersensitivity;
                                                                                                                555
                                                                                                                                                                                                                                          0
                             mite allergen protein (map)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뜆
                                                                                                                                                                                                                                                         Score 78;
Pred. No.
                                                                                                                A
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                       6.4e-05;
                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                           <u>.</u>
                                                                                                                                                                                                                                                                      Length 536;
                                                                                                                                                                                                                                           Indels
                              PDerf98-555
                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                           Gaps
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Claim 3; Page 111-113; 154pp; English.

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17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fel canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                              Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                      N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
                                                                                                                                                                                                                                                                                                                      16-APR-1999;
                                                                                                                                                                                                                                                                                                                                     28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                      WO9954349-A2
                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                        Key
Yey
                                                                                                                                                                                                                                                                                                                                                                                                                      Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                  (HESK-) HESKA CORP.
                                                                                                                                                                                                                                 2000-052700/04.
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98US-0085295P.
98US-0098909P.
                                                                                                                                                                                                                                                                                                                      99WO-US008524.
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      /note= "Mature PDerf98-555"
                                                                                                                                                                                                                                                                                                                                                                                     /note= "Signal
                                                                                                                                                                                                                                                  WS.
                                                                                                                                                                                                                                                                                                                                                                                . 555
                                                                                                                                                                                                                                                   Weber
                                                                                                                                                                                                                                                                                                                                                                                       peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; feline;
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CT This sequence represents Dermatophagoides farinae mite allergen protein CC (map) pDerf98-555. pDerf98-555 has a molecular weight of 98 kD, comprising 555 amino acids, and is a component of the Dermatophagoides CC farinae high molecular weight mite allergen protein (HMM-map) molecular weight mite allergen protein farinae CC composition. The HMM-map composition was isolated from a D. farinae CC composition. The HMM-map composition was isolated from a D. farinae CC presence of proteins that bound to 19E present in mite-allergic dog CC antisera. Mite allergenic proteins and peptides, and nucleic acids CC encoding them, may be used in therapeutic compositions to modify an CC animal's hypersensitivity reaction to mite allergens. Animals that may be used to mite allergens. Animals that may be continued in the proteins or CC treated include mammals and birds, especially felines, canines, equines, CC proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to positive controls in test kits and as tools to recover desired dust mite to the controls in test kits and as tools to recover desired dust mite to the controls and peptides can also be used to raise antibodies, which have a controls in test kits and as tools to recover desired dust mite to the controls in test kits and as tools to recover desired dust mite to the controls of proteins of proteins.

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Sequence 555 AA;
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RESULT 8
AAU96327
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SEXEXE
BXXXXX
                                                                                                              Query Match
Best Local
                                                                                                       Matches
                      AAU96327;
                                   AAU96327
                                                                                                              Local
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                                                                                                       14;
                                                                                                              Similarity
                                                                          SIKRDHNDYSKNPM
                                                                                        SIKRDHNDYSKNPM 14
                                    standard;
                                                                                                      100.0%; ilarity 100.0%; Conservative 0
                                    protein;
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                                     5
5
5
                                                                                                      0;
                                                                                                               Score 78;
Pred. No.
                                                                                                       Mismatches
                                                                                                               6.7e-05;
                                                                                                                      DB 3;
                                                                                                                     Length 555;
                                                                                                        Indels
                                                                                                        0
                                                                                                        Gaps
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0

15-501-2002

(first entry)

Der HMW-map

polypeptide

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RESULT 9
AAU96328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC detection of anti-Der HMW-map protein and its related nucleic detection of anti-Der HMW-map protein is useful for eliciting an immune response call susceptible to or having an allergic response to a mite. The DNA and protein an immune response community of a mite and the response composition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the categories of anti-Der HWW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWW-map protein activity associated with a categories. Antibodies that bind to Der HWW-map are useful for inhibition complexes, antibodies that bind to Der HWW-map are useful for inhibiting composition of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWW-map polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                             AAU96328 standard; protein; 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated mite allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 114-116; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Der HMW-map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-351888/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunocomplex formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Der HMW-map; American
                                              Dermatophagoides farinae
                                                                              mite allergenic immunocomplex fo
                                                                                            Der HYW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                            Der HMW-map polypeptide #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HESK-) HESKA CORP
                                                                                                                                                                                15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                 SIKRDHNDYSKNPM 33
                                                                                                                                                                                                                                                                                                                                                              SIKRDHNDYSKNPM 14
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hunter SW,
                                                                                                                                                                                (first entry)
                                                                                formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house dust mite; antiallergic; mite; IgE; in; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weber ER;
                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78; DB 5;
Pred. No. 6.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    0
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RESULT 10
AAY52535
ID AAY52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated mite allergenic protein of CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic CC acid. The Der HMW-map protein is useful for eliciting an immune response eagainst Der HMW-map protein. The protein or a reagent comprising a non-cc proteinaceous epitope is useful for identifying an animal (e.g., dog, CC act) susceptible to or having an allergic response to a mite. A cC therapeutic composition is useful for desensitising a host animal to an CC disease to a mite. The DNA and protein can be used in the CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting CC binding of proteins to IgE, to prevent immunocomplex formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANU96314-AAU96342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                   06-AUG-2003
22-FEB-2000
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                                                                                                                                                                                                 Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 120-122; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-351888/38
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                                                                                                                                                                                                                                                         D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490
                                                                                                                                                                                                                                                                                                                               AAY52535;
                                                                                                                                                                                                                                                                                                                                                           AAY52535 standard; protein; 490 AA
                                                                                                                                                       Dermatophagoides pteronyssinus
                                                                                                                                                                                   canine; veterinary; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HESK-) HESKA CORP
                                                                                    Modified-site
                                                                                                              Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US028730
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                  (revised)
                                                                                  240.
                                                                        /note= .
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                                                                                                                          Location/Qualifiers
                                                                                               "Asn is N-glycosylated"
                                                                     "Asn is N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 78; DB
Pred. No. 6.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; 1
                                                                                                                                                                                      immunisation
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28-OCT-1999

WO9954349-A2

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This sequence represents Dermatophagoides preronyssius mite allergen comportein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490 composition of the polyment of the polyment of the polyment of polyment of polyments and has a composition of the polyment of the polyment of polyment 
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Matches
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13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU96339 standard; protein; 490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 147-149; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1999;
                                                                                                                                                                                                                                                                                                                                         Der HMW-map polypeptide #26.
                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HESK-) HESKA CORP
                                                                                                                                                                                                              Dermatophagoides
                                                                                                                                                                                                                                                                              Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                               21-MAR-2002
                                           14-SEP-2000; 2000US-00662293
                                                                                     14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                                          immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-052700/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ38589,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRDHNNYSKNPM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRDHNDYSKNPM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00062013.
98US-0085295F.
98US-0098909F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US008524.
                                                                                                                                                                                                                   farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ38590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.3%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        덝
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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HESKA

(HESK-) HESKA

CORP

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RESULT 12
AAY52533
ID AAY52533
AX AAY52533
AX AAY5253
AX AAY52
AAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           against Der HMW-map protein. The protein or a reagent comprising a non-
proteinaceous epitope is useful for identifying an animal (e. gr., dog,
cat) susceptible to or having an allergic response to a mite. A
therapeutic composition is useful for desensitising a host animal to an
allergic response to a mite. The DNA and protein can be used in the
detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
of immunoglobulin (1g) or Der HMW-map protein activity associated with a
disease. Antibodies that bind to Der HMW-map are useful for inhibiting
binding of proteins to IgB, to prevent immunocomplex formation, thus
reducing hypersensitivity responses to mite allergens, and as vaccines
against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an Dermatophagoides, designated acid. The Der HMW-map protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mccall CA,
                                                  17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

    D. pteronyssius

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22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY52533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY52533 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mite allergenic protein isolated from Dermatophagoides, designa
Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                canine; veterinary; antibody;
                                                                                                                                                                                                                     28-OCT-1999.
                                                                                                                                                                                                                                                                              WO9954349-A2
                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dermatophagoides pteronyssinus
                                                                                                                                                                   16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-351888/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KRDHNDYSKNPM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRDHNNYSKNPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agoides, designated Der HMW-map protein, and its related nuclei
Der HMW-map protein is useful for eliciting an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 144-146; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hunter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                     98US-00062013.
98US-0085295P.
98US-0098909P.
                                                                                                                                                                     99WO-US008524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 kD mite allergen protein (map) PDerp98-509
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   /note= "Mature PDerp98-509"
                                                                                                                                                                                                                                                                                                                                                                                   /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                               .509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated mite allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        띯
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and its related nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    designated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 13
AAU96337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC protein (map) Derry98-509. Pherp98-509 has a molecular weight of 98 kb, comprising 509 amino acids, and has a high degree of homology with the D. CC farinae 98 kb allergen, mapB (AAY55523). Nucleic acid molecules encoding PDerry98-509 were isolated from a D. pteronyssius cDNA library by CC phyridisation with a probe encoding the D. farinae high molecular weight map (HMW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to comdify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, CC canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as C vaccines to passively immunise animals against dust mite allergens from a mixture of proteins. (Updated con 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                         AAU96337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU96337 standard; protein; 509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 134-136; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ38585,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccall CA,
                            WPI; 2002-351888/38.
N-PSDB; ABK69581.
                                                                                                                                                                                                                                                                Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                              Der HMW-map; American house dust mite; antiallergic; mite; IgE;
                                                                                                                                                                                                                                                                                                                                                            Der HMW-map
                                                                                                                                                                                                      21-MAR-2002
                                                                                                                                                                                                                                    WO200222807-A2
                                                                                                                                                                                                                                                                                                                mite allergenic protein;
New mite allergenic protein isolated from Dermatophagoides, designated
                                                                            Mccall CA,
                                                                                                                                        14-SEP-2000; 2000US-00662293
                                                                                                                                                                      14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                                                                                 immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-052700/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRDHNNYSKNPM 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRDHNDYSKNPM 14
                                                                                                                                                                                                                                                                                                                                                           polypeptide #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hunter SW,
                                                                              Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represents Dermatophagoides pteronyssius mite allergen
                                                                                                           CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ38586, AAZ38587, AAZ38588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weber ER
                                                                              Weber
                                                                                                                                                                                                                                                                                                              immunoglobulin E; hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 3; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 14
AAU96338
ID AAU96
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease, Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an therapeutic composition is useful for desensitising a host animal to an
                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                         Der HMW-map; American house mite allergenic protein; imm immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Der HMW-map protein, useful as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Der HMW-map polypeptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU96338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU96338 standard; protein;
                                                                                                                         New mite allergenic pler HMW-map protein,
                                                                                                                                                                                                             Mccall
                                                                                                                                                                                                                                                                                                14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                                                                                                                                                                       WO200222807-A2
                                                                                                                                                                                                                                                                                                                                                                                 Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2002
                                                                                               Claim
                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                   14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                          (HESK-) HESKA CORP
                                                                                                                                                                   2002-351888/38.
DB; ABK69583.
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                                                                                                                                                                                                               Hunter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                               139-141;
                                                                                                                                                                                                               WS.
                                                                                                                         protein isolated from Dermatophagoides, useful as a vaccine for treating mite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.3%;
91.7%;
                                                                                               161pp;
                                                                                                                                                                                                               Weber
                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB Pred. No. 0.01; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                           antiallergic; mite; I
n E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mite allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related nucleic
                                                                                                                            allergy.
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for a reagent minmune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A

its related nucleic

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ARBSULT 15
AAB94676
ID AAB94
XX AAB94
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XX 29-UI
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T,
Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000EP-00116126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein sequence SEQ ID NO:15624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2001
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                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
   sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID NO 15624; 2537pp + Sequence Listing; English
                                                                                                                               of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
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, Sugiyama
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; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00248036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa T,
T, Wakamatsu
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Pred. No. 0.011;
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A, Nagai K,
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Best Local &
                                                                                                                                                                                      specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13638 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification of the
                                                                                                                                         Sequence 445 AA;
                                                                                                                                                                           present invention
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                                                                    Similarity 7; Conserv
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Search completed: March 22, 2004, 06:51:32
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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### ALIGNMENTS

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TITLE OF INVENTION: MOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROFITITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,225
EARLIER APPLICATION NUMBER: 60/098,525
EARLIER APPLICATION NUMBER: 60/098,525
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
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US-09-292-225-1
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               Sequence 24, Application US/09292225
PATENT NO. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES,
FILE REFERENCE: ALC-2-C3
FILE REFERENCE: ALC-2-C3
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APPLICANT: McCall, Catherine &
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
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LENGTH: 14
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CURRENT APPLICATION NUMBER: US/09/292,225
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CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
UNMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
LENGTH: 536
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US-09-292-225-21
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EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
MUMBER OF SEQ ID NOS: 49
NUMBER OF SEQ ID NOS: 49
NUMBER OF SEQ ID NOS: 49
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SEQ ID NO 24
LENGTH: 33
                Sequence 15, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Dermatophagoides farinae
-09-292-225-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
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No. 645568,
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100.0%; Pred. No. 9.2e-06;
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-15
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
COMMUNICATION OF SEQ ID NOS: 49
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CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 199-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
NUMBER OF SEQ ID NOS: 49
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US-09-292-225-18
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SEQ ID NO 15
LENGTH: 555
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SEQ ID NO 18
LENGTH: 555
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Patent No. 6455686
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Best Local Similarity
                                                                                  Matches
                                                                                                        Query Match
Best Local
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Heber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
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APPLICANT: Weber, Eric R.
                                                                                                                                                                                                              LENGTH: 55
TYPE: PRT
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                                                                                  Local Similarity hes 14; Conserv
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RESULT 6
US-09-292-225-41
; Sequence 41, Application US/09292225

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US-09-292-225-35
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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Best Local
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                                                                                          Matches
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ORGANISM: Dermatophagoides farinae
-09-292-225-41
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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FILING DATE: 1999-04-15
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91.7%;
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Pred. No. 0.0016;
1; Mismatches
                                                                                                               Score 65; DB 4;
Pred. No. 0.0017;
                                                                                            Mismatches
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                                                                                                                                       Length 509;
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RESULT 10
US-09-252-991A-25153
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                                                                                                                                                                                                                                          ; ORGANISM: Proteus mirabilis US-09-543-681A-7570
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7570, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DUCKIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7570
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LENGTH: 509
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GENERAL INFORMATIC
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Best Local Similarity
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/095,295
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
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EARLIER FILING DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                  LENGTH: 121
TYPE: PRT
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                                                                                                                       SIKRDHNDYSKN 12
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                                                                                                                                                             Conservative
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91.7%;
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Pred. No. 0.00
1; Mismatches
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Pred. No. 5.
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Sequence 25153, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:

APPLICANT:

Marc J.

Rubenfield et al

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/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25153

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US-09-252-991A-24219
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24219
                                                                                                                                                  SEQ ID NO 25153
LENGTH: 820
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LENGTH: 150
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Best Local
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CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US/09/064,964

PRIOR PILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US/09/064,964

PRIOR APPLICATION NUMBER: US/09/055,779
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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NUMBER OF SEQ ID NOS: 5674
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Local Similarity 46.2%;
hes 6; Conservation
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41.7%;
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Pred. No.
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Pred. No. 1.1e+02;
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APPLICANT: Sturgis, Blake
TITLE OF INVENTION: Pesticidal Toxins and Ge
TITLE OF INVENTION: Strains
FILE REFERENCE: MA-719XC2D1
CURRENT APPLICATION NUMBER: US/09/967,805
CURRENT FILING DATE: 2001-99-28
PRIOR APPLICATION NUMBER: 09/371,913
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/095,955
PRIOR APPLICATION NUMBER: 60/138,251
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/138,251
PRIOR FILING DATE: 1999-06-08
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Best Local Similarity 46.2%;
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SEQ ID NO 7
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Patent No. 660570
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TITLE OF INVENTION: Pesticidal Toxins and Genes from Bacillus laterosporus
TITLE OF INVENTION: Strains
FILE REFERENCE: MA-719xC2 US
CURRENT APPLICATION NUMBER: US/09/371,913A
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/095,955
PRIOR PELING DATE: 1998-08-10
PRIOR PILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/138,251
PRIOR FILING DATE: 1999-06-08
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                   APPLICANT: Schnepf, Ernest H
APPLICANT: Narva, Kenneth E
APPLICANT: Stockhoff, Brian A
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Peptide sequence
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Pred. No.
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Pred. No.
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Sequence 2, Application US/09719190

Patent No. 6649171

GENERAL INFORMATION:

APPLICANT: Thomnard, Joelle

TITLE OF INVENTION: Moraxella Catharrahalis Polynucleotides

TITLE OF INVENTION: and Polypeptides

FILE REFERENCE: BM45326

CURRENT APPLICATION NUMBER: US/09/719,190

CURRENT FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: PCT/EP99/03824

PRIOR APPLICATION NUMBER: PCT/EP99/03824

PRIOR FILING DATE: 1999-05-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 947

TYPE: PRT

ORGANISM: Moraxella catarrhalis

US-09-719-190-2
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Peptide sequence
US-09-967-805-7
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Search completed: March 22, 2004, 07:03:52 Job time: 1.1284 secs
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US-09-719-190-2
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758 QDYNNYSKN 766
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Result
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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seq length: 2000000000
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1479.047 Million cell updates/sec
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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T13181
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serine/threonine	pyruvate-formate	probable glutamine	hypothetical prote	L-lactate dehydrog	venombin	hypothetical	snake venom	snake venom	protein F02C9.4	guanylin precursor	AcOrf-150 protein	hypothetical prot	xylan	cation-transportin	D. C. C. L.

#### ALIGNMENTS

RESULT 1 T14075

A;Status: preliminary; translated from GB/EMBL/DDB:

A; Accession: T14075

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R;Kodaira, K.I.; Oki, M.; Kakikawa, M.; Watanabe, N.; Hirakawa, M.; Yamada, K.; Taketo, Gene 187, 45-53, 1997
A;Title: Genome structure of the Lactobacillus temperate phage phi gle: the whole genom A;Reference number: Z17631; MUID:97225795; PMID:9073065
A;Accession: T13181
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                           RESULT 2
T13181

T13181

C;Species: Lactobacillus phage phi-gle
C;Species: Lactobacillus phage phi-gle
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C;Accession: T13181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-1635 <DEL>
A;Cross-references: EMBL:AF026492; NID:g2564720; PID:g2564721;
C;Genetics:
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                                                                               A;Gene:
                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-66 < KOD>
                                                                                                                 A;Cross-references: EMBL:X98106; NID:e917136; PID:e247183; PIDN:CAA66757.1
Query Match
Best Local S
Matches 9
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Best Local 9
                                                                                                 Genetics:
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1134 VPHPTDCNKYYICQ 1147
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                   Similarity
   Conservative
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hydrolase; polysaccharide
                     46.5%;
 Score 53.5; DB Pred. No. 0.28; 4; Mismatches
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DIPHPTNI - - - HKYLVCE

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C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_c
C;Accession: T44445
R;Shen, Z: J Jacobs-Lorena, M.
submitted to the EMBL Data Library, June 1997
A;Reference number: Z22771
A;Accession: T44445
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-525 cSHE-
A;Cross-references: EMBL/AF008575; PIDN:AAB87764.1
                                                                                                                                                                                                                                                                                                                                                                                                                              Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1136
A;Accession: AC1136
A;Accession: AC1136
A;Status: preliminary
A;Accession: Proper DNA
A;Residues: 1-291 «GLA»
A;Residues: 1-291 «GLA»
A;Cross-references: GB:NC 003210; PIDN:CAC98569.1; PID:g16409866; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Gene: Im00490
C;Superfamily: shikimate 5-dehydrogenase; shikimate dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shikimate 5-dehydrogenase homolog lmo0490 [imported] - Listeria monocytogenes (;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 07-Jul-2003 C;Accession: AC1136 C;Accession: AC1136 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: chi-1
C;Keywords: glycosidase; hydrolase
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shikimate 5-dehydrogenase homolog lin0493 [imported] - Listeria innocua (strain C;Species: Listeria innocua (strain C;Species: Listeria innocua (c;Spacies: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 07-Jul-2003 C;Accession: AE1494 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; ;; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F
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                                                                                                                                                AE1494
                                                                                                                                                                        RESULT
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8; Conserv
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nilarity 72.7%;
Conservative ;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                             Score 47; DB
Pred. No. 13;
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2.8;
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Fsihi, H.
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Fsihi, H.
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                                                                                                                                                                     RESULT 7
VGBE37
  glycoprotein H - human herpesyirus 3
N,Alternate names: glycoprotein III
C,Species: human herpesyirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #tex
C;Accession: B27341
R;Davison, A.J.; Scott, J.E.
R;Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1494
                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X82444; NID:g563910; PIDN:CAA57824.1; PID:g563911
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, submitted to the EMBL Data Library, July 1999
A;Reference number: Z21880
A;Accession: T39793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S53990; T39793
R;WilKinson, C.R.M.; Barrlett, R.; Nurse, P.; Bird, A.P.
Nucleic Acids Res. 23, 203-210, 1995
A;Title: The fission yeast gene pmt1(+) encodes a DNA methyltransferase
A;Reference number: S53990; MUID:95166638; PMID:7862522
A;Accession: S53990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: lin0493
C;Superfamily: shikimate 5-dehydrogenase; shikimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL592022; PIDN:CAC95725.1; A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                   C; Superfamily: site-specific methyltransferase
                                                                                                                                                                                                             A; Map position:
                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-330 <MCD>
A;Residues: 1-330 <MCD>
A;Residues: 1-350 <MCD>
A;Residues: GSPDB:GN00067; SPDB:SPBC19C2.02
A;Experimental source: strain 972h-; cosmid c19C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-330 < WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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A;Residues: 1-291 <GLA>
                                                                                                                                                                                                                                   A;Gene: SPBC19C2.02
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                                                                               Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Schizosaccharomyces pombe;Date: 15-Jul-1995 #text_change 17-Mar-2000;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-2000;Accession: S53990; T39793
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Best Local
108 LPHVNNLPEYILIENVQG
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125
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Pred. No. 15;
6; Mismatches
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                                                                                                                                                                   (cytosine-specific)
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Voss, H.; V
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Wehland,
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#text\_change 16-Jul-1999

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A;Gene: 37
C;Superfamily: herpesvirus glycoprotein H
C;Keywords: glycoprotein
C;Keywords: glycoprotein
F;18,45,83,217,317,499,522,560,760,783/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The complete DNA sequence of varicella-zoster virus. A;Reference number: A27345; MUID:86306657; PMID:3018124 A;Accession: B27341 A;Molecule type: DNA A;Residues: 1-841 <DAV> A;Residues: 1-841 <DAV> A;Coss-references: EMBL:X04370; NID:g59989; PIDN:CAA27920.1; C;Genetics:
                                                                                                                A;Cross-references: EMBL:AL031534; PIDN:CAA20726.1; A;Experimental source: strain 972h-; cosmid c4F6
                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-891 < GWI>
                                                                                                                                                                                      submitted to the EMBL Data Library, A;Reference number: Z21933
A;Accession: T40503
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R;Gwilliam, R.; Rajandream,
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C;Superfamily: CTP synthase
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A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
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Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                         Species: Schizosaccharomyces pombe;Date: 03-Dec-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14837.1;
;Experimental source: strain Madrid E
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Date: 21-Nov-1998 #sequence_revision
                                                         ;Superfamily:
                                                                                     ;Gene: SPDB:SPBC4F6.06
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40.0%; ilarity 60.0%; Conservative
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Score 46; DB
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2; Mismatches
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          DB
58;
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Rilevin, D.E.; Bishop, J.M.
Rilevin, D.E.; Bishop, J.M.
RenBank, May 1991
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C;Species: Schizosaccharomyces pombe
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                 A; Reference number: Z15454
A; Accession: T05842
                                                                                                                                                                                                                                                                                                                          R;Bevan, M.; Van Der Schueren, J.; submitted to the Protein Sequence
                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F17L22.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 13-Aug-1999
                                                                                                                                           A;Map position: 4
A;Introns: 106/3;
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A; Residues: 1-361,'R',363-619,'I',621-707,'W',709-891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A36474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: A putative protein kinase gene (kin1(+)) is im A;Reference number: A36474; MUID:91045979; PMID:2236039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Levin, D.E.; Bishop, J.M. Proc. Natl. Acad. Sci. U.S.A. 87, 8272-8276,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A38903
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                                                                                                                                                                                                                      A;Residues: 1-995 <BEV>
A;Cross-references: EMBL:AL035527
                                                                                                                                                                                                                                                               A; Molecule type: DNA
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A;Residues: 1-891 <LEV>
                                                                                                                                                                                                    Experimental source: cultivar Columbia; BAC clone F17L22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: unassigned Ser/Thr or Tyr-specific protein kinas
;Keywords: ATP; phosphotransferase; serine/threonine-specific
;Keywords: ATP; protein kinase homology <KINs
;131-139/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: nucleic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GB:M64999; NID:g173409; PIDN:AAA63577.1; PID:g173410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Reference number: A38903
                                                                                                                        F17L22.130
                                        Similarity
9; Conser
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DIPHPTNIHKYLVCESVNGG 20
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                                                                                                                                        265/3; 350/1; 402/3; 425/2;
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                                                      40.0%;
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Pred. No. 58;
2; Mismatches
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ATP-binding motif
                                   Score 46; DB Pred. No. 65; 2; Mismatches
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                                                    DB
65;
                                                                                                                                                                                                                                                                                                                       r.J.; Voet, M.; Robben, J.; Volckaert, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1990
                                                                                                                                           460/3; 488/3; 690/3;
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AcMNPV orf150 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C;Species: Bombyx mori nuclear polyhedrosis virus, Bm6NPV

A;Variety: isolate T3

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000

C;Accession: T41887

R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen, Virol. 80, 1323-1337, 1999

A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A;Accession: T41887

A;Accession: T41887
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T41887
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A;Residues: 198-342 «WOO»
A;Cross-references: EMBL:AL035077; PIDN:CAA22661.1; GSPDB:GN00066; SPDB:SPBC18E5.
A;Experimental source: strain 972h-; cosmid c18E5
C;Genetics: <-LYN1>
C;Genetics: <-LYN1>
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A;Molecule type: DNA
A;Residues: 1-342 < LYN>
A;Residues: 1-342 < LYN>
A;Cross-references: EMBL:AL022299; PIDN:CAA18396.1; GSPDB:GN00067; SPDB:SPBC29A3.19
A;Cross-references: strain 972h-; cosmid c29A3
A;Experimental source: strain 972h-; cosmid c29A3
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.; Xiang, Z.; Aves, S.
submitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z21904
A; Accession: T40090
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A;Note: Orf_126
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A; Residues: 1-115 < KAM>
A; Cross-references: EMBI
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C; Genetics: <WOOl>
chitinase (EC 3.2.1.14) MF1 - nematode (Brugia malayi)
C;Species: Brugia malayi
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #te
                                                                           RESULT 14
A38221
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A;Accession: T39752
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Best Local
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Best Local (
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                                                                                                                                                                   PHPTKCNAFYMCVGIN 75
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llarity 37.5%;
Conservative
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:e: isolate T3
  #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
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55.6%;
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Pred. No. 26
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Pred. No. 10;
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Search completed: March 22, 2004, 07:01:19
Job time: 3.30072 secs

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C;Accession: A38221
R;Fuhrman, J.A.; Lane, W.S.; Smith, R.F.; Piessens, W.F.; Perler, Proc. Natl. Acad. Sci. U.S.A. 89, 1548-1552, 1992
A;Title: Transmission-blocking antibodies recognize microfilarial A;Reference number: A38221; MUID:92179220; PMID:1542646
A;Accession: A38221
                                                                                                                                                                                                                                                                                                                       R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 199

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84732
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A;Residues: 1-504 <FUH>
A;Residues: 1-504 <FUH>
A;Cross-references: GB:M73689; NID:g156063; PIDN:AAA27854:1; PID:g156064
A;Note: sequence extracted from NCBI backbone (NCBIP:85345)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable ubiquitin activating enzyme [imported] - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84732
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A; Residues: 1-523 <STO>
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                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
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position: 2
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    PSTTELHKYLADENYSG
                                          PHPTNIHKYLVCESVNG
                                                                                       Conservative
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Pred. No.
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Pred. No.
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46;
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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115
1 DIPHPTNIHKYLVCESVNGG
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   SwissProt_42:*
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   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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PST_SCHPO
VGH_VZVD
PST_ARCCA
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KINI_SCHPO
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YBS1_SCHPO
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p45442 caenorhabdi

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Q75676 homo sapien

Q83218 treponema p

Q13063 trimeresuru

Q25113 hemicentrot

p23298 mus musculu

Q64617 rattus norv

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A. Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
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A. Gautier L., Goebel W., Gomez-Lopez N., Hain T., Kunst F., Kurapkat G.,
A. Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A. Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
A. Madueno E., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A. Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A. Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294 849-852 (2001).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Shikimate 5-dehydrogenase (EC 1.1.1.25).
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MEDLINE=21537279; PubMed=11679669;
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Bacteria; Firmicutes;
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Q8-FBB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Shikimate 5-dehydrogenase (EC 1.1.1.25).

AROE OR IMO0490:
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Chavcuani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
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PIR; AC1136; AC1136.
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RESULT 4
PMT1\_SCHPO
ID PMT1\_SCHPO

STANDARD

PRT;

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RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S. McDonald S., McLean J., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA James K., Jones J., Jones M., Leather S., McDonald S., McLean J., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA McOrer K., Rutter S., Saunders D., Seeger K., Sharp S., Ra McLearford K., Rutter S., Squares R., Squares K., Stevens K., Ra Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Ra McLeard J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Rieger M., Schaefer M., Mueller-Auer S., Ra Woodward J., Volckaert G., Rieger M., Schaefer M., Mueller-Auer S., Ra Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Ra Gorzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Machaer M., Westery D., Barrell B.G., Nurse P., and Machaer M., Ussery D., Barrell B.G., Nurse P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P40999;
01-FEB-1995
01-FEB-1995
                                                                                                                 the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I
                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96194447; PubMed=8636983;
Pinarbasi E., Elliott J., Hornby D.P.;
"Activation of a yeast pseudo DNA methyltransferase by deletion of single amino acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Pota
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA methyltransferase PMT1 OR SPBC19C2.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilkinson C.R.M.,
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                                                                                                                                                                                                                                                                                                             it becomes catalytically active and recognizes and methy sequence CC[AT]GG.
SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Belongs to the C5-methyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Does not have a cytosine-5 methyltransferase activity due to the insertion of a Ser residue between the Pro-Cys motif found at the active site of C5 MTases. When this serine is deleted the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ol. Biol. 257:804-813(1996). FUNCTION: Does not have a cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acids Res. 23:203-210(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gwilliam
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                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a DNA methyltransferase
                                                                                                                                                  There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyne M., Lyne R.,
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                                                                                                                 Usage
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RESULT 5
VGLH_VZVD
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        Query Match
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InterPro; IPR001525; C5 DNA meth.
Pfam; Pr00145; DNA methylase; 1.
PRINTS; PR00105; C5METTRPRASE;
PROSITE; PS00094; C5 MTASE 1; FALSE
PROSITE; PS00095; C5 MTASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL10973
PIR; S53990;
HSSP; O14717;
                                        CARBOHYD
CARBOHYD
SEQUENCE
                                                                       CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
                                                                                                                                                           PIR; B27341; Glycoprotein;
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Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable glycoprotein H precursor (Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear SITE 81 8
SEQUENCE 330 AA; 3
                                                                                                                                                                               EMBL;
                                                                                                                                                                                                  entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     nse
                                                                                                                                                                                                                                                                                    "The complete DNA sequence of varicella-zoster virus.";
J. Gen. Virol. 67:1759-1816(1986).
-!- SIMILARITY: Belongs to the herpesviruses glycoprotein H
                                                                                                                                                                                                                                                                                                                     MEDLINE=86306657; PubMed=3018124; Davison A.J., Scott J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P09260
                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; 014717; 1G55.
REBASE; 2888; M.SpomI
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UVZV
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                                                                                                                                                                               X04370;
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7; Conserv
8
         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                               CAA27920.1;
                                                                                                                                                            Transmembrane;
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37976 MW;
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50.0%;
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Pred. No. 4.2;
6; Mismatches
        Score 47;
Pred. No.
                                                   N-LINKED
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N-LINKED
N-LINKED
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                                                                                                                                     Signal.
POTENTIAL.
PROBABLE GLYCOPROTEIN H.
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 Mismatches
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12;
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                  Length 841;
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Matches 7
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SIGNAL 1 17 PC
CHAIN 18 153 PC
DOMAIN 18 79 CH
DOMAIN 92 153 CH
CARBOHYD 63 63 N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A type I peritrophic matrix protein from the malaria vector Anopheles gambiae binds to chitin. Cloning, expression, and characterization.";
J. Biol. Chem. 273:17665-17670 (1998).

- I- FUNCTION: Binds chitin but not cellulose. May be involved in the spatial organization of PM.

- I- TISSUE SPECIFICITY: Adult peritrophic membrane.

- I- DEVELOPMENTAL STRAGE: Expressed in adult but not larval guts, whole gupae or whole bodies minus gut.

- I- PTM: Glycosylated.
                                                                Q9ZDF1;
16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                             CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF030431; AAC39127.1; -
InterPro; IPR002557; Chitin_bind_PerA.
Pfam; PF01607; CBM 14; 2.
SMART; SM00494; ChTBD2; 2.
PROSITE; PS50940; CHIT_BIND_II; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEI_ANOGA STANDARD; PRT; 153 AA (776217; 777217)
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Ano
            Rickettsia
Bacteria; F
                                      CTP synthase
PYRG OR RP378
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF030431; AAC39127.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7165;
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STRAIN=G3; TISSUE=M
                                                                                                                      PYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 2 chitin-binding type-2 domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration -
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7; Conserv
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                                                                                                                                                                                      IPHETDCCKYYICD 120
         a prowazekii.
Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                                                                                          18
18
18
92
63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Midgut;
                                                 (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
(EC 6.3.4.2) (UTP--ammonia ligase)
                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                             ΑĀ,
                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                              16819 MW;
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                                                                                                                                                                                                                                                     Score 46;
Pred. No.
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CHITIN-BINDING TYPE-2 2.
N-LINKED (GLCNAC. . .) (PC,
2218DA0310476338 CRC64;
                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PERITROPHIN-1.
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                                                                                                                                                                                                                                                                                                                                                                         Signal.
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RESULT KIN1\_SC ID KI AC P2

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HAMAP; MF 01277; atypical; 1.
InterPro; IPR000991; GATase_1.
InterPro; IPR004468; PyrG_synth.
InterPro; IPR005728; Rickett_RPE
                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raoult D., Claverie J.-M.;
"Selfish DNA in protein-coding genes of Rickettsia.";
Science 290:347-350(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.l
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Madrid E;
MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsiaceae;
NCBI_TaxID=782;
                                                                                                                                                                                                  TICKFAMS; TICK00337; PyrG; 1.
TICKFAMS; TICK01045; RPE; 1.
PROSITE; PS00442; GATASE_TYPE_I; 1.
Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raoult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20485642; PubMed=11030655;
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                         Complete
                                                                                                                                                                                                                                                        Pfam; PF00117; GATase; 1.
                                                                                                                                                                                                                                                                                                                                 EMBL; AJ235271; CAA14837.1; -.
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                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotetramer (By similarity).
SIMILARITY: Belongs to the CTP synthase family.
SIMILARITY: Contains 1 type-1 glutamine amidotr
SIMILARITY: Contains 1 RPE1 insert domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; third
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phos
ENZYME REGULATION: Allosterically activated by GTE
is the substrate. Inhibited by CTP (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
CATALYTIC A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Catalyzes the ATP-dependent
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115
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                                                Similarity 50. 9; Conservative
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Claverie J.-M.;
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GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
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                                                Score 46; DB Pred. No. 11; 2; Mismatches
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                                                                                                                                                                 GLUTAMINE AMIDOTRANSFERASE
                                                                                                                                                                             AMINATOR DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of UTP to
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DAN BERRARA BE
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RA Bgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Kelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Roboward J., Volckaert G., Aert R., Squares S., Stevens K.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Moodward J., Volckaert G., Aert R., Mobben J., Grymonprez B.,
RA Gerber M., Teles E., Rieger M., Schaefer M., Mueller R.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cohet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Mocseno S., Armstrong J., Forsburg S.L.,
RA Cerritti L., Lowe T., McCombie W.R., Paulsen I., Pottaskkin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levin D.E., Bishop J.M.;
"A putative protein kinase gene (kin1+) is important polarity in Schizosaccharcomyces pombe.";
Proc. Natl. Acad. Sci. U.S.A. 87:8272-8276(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.",
Nature 415.871-880(2002).
-!- FUNCTION: Probable serine/threonine protein kina
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROSTRONG, TO YEAST KIN1 AND KIN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel.
16-OCT-2001 (Rel.
28-FEB-2003 (Rel.
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Wood V., Gwilliam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomycetales; Schizosaccharomycetaceae;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                        PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Use this entities requires a license agreement (See htter
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MEDLINE=91045979; PubMed=2236039;
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T40503; T40503.
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o; IPR001772; Kinase
o; IPR000719; Prot_kinase.
j; IPR008271; Ser_thr_pkin_AS.
j; IPR0022290; Ser_thr_pkinase.
j; IPR0022245; Tyr_pkinase.
702149; KA1; 1.
700069; pkinase; 1.
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R., Rajandream M.A.,
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Q968X7;
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Probom; PD000001; Prot kinase; 1.

SMART; SM00220; STOTEIN KINASE ATP; 1

PROSITE; PS00109; PROTEIN KINASE ST; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                     MBDLINE=21219183; PubMed=11319255; Rotte C., Stejskal F., Zhu G., Keithly J.S., Martin W.; Rotte C., Stejskal F., Zhu G., Keithly J.S., Martin W.; "Pyruvate: NADP oxidoreductase from the mitochondrion of Euglena gracilis and from the apicomplexan Cryptosporidium parvum: A biochemical relic linking pyruvate metabolism in mitochondriate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cryptosporidium parvum.
Eukaryota; Alveolata; F
Cryptosporidiidae; Cryp
                                                                             This
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                                                                                                                                                                                                                                                                                                                                                         amitochondriate protists.";
Mol. Biol. Evol. 18:710-720(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxidoreductase)
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no waified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                           FUNCTION: May have an important role in respiratory metabolism. Cryptosporidium have a relic mitochondrion with no function in energy metabolism so it is not known if PFOR has a function. CATALYTIC ACTIVITY: Pyruvate + COA + NADP(+) = acetyl-COA + CO(2)
                                                                                                        MISCELLANBOUS: Arose from gene fusion of pyruvate:ferredoxin oxidoreductase and cytochrome-P450 reductase. Gene fusion has been found in Euglena and Cryptosporidium.

SIMILARITY: The irron-sulfur centers are similar to those of bacterial-type 4Fe-4S ferredoxins.

SIMILARITY: Contains 1 flavodoxin-like domain.
                                                                                                                                                                                                                                and one FAD per chain SUBUNIT: Homodimer (By
                                                                                                                                                                                                                                                                COFACTOR: Thiamine pyrophosphate. Flavoprotein
                                                                                                                                                                                                                  DEVELOPMENTAL STAGE:
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004 (Rel. 43, Last annotation update)
004 (Rel. 43, Last annotation update)
dehydrogenase [NADP+] (EC 1.2.1.51)
uctase) (CpPNO).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e; Serine/threomine-protein kinase; ATP-b
125 395 PROTEIN KINASE.
131 139 ATP (BY SIMILARITY).
154 154 ATP (BY SIMILARITY).
266 266 BY SIMILARITY.
266 266 BY SIMILARITY.
141 V -> D (IN REF. 1).
247 247 V -> E (IN REF. 1).
620 620 I -> N (IN REF. 1).
620 620 IR -> ML (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            891 AA;
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131
141
141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ca; Apicomplexa;
Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.0%;
60.0%;
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                                                                                                                                                                                                                  (By similarity)
3: Both sporozoi
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Pred. No.
                                                                                                                                                                                                                    sporozoites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89D9BB6D825C0358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coccidia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eimeriida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Pyruvate:NADP+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding.
                                                                                                                                                                                                                    intracellular stages
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
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                                                               collaboration
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RESULT 10
YBS1_SCHPC
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Best Local S
Matches
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Pfam; PF00237; fer4; 2.

Pfam; PF00238; flavodoxin; 1.

Pfam; PF00175; NAD binding_1; 1.

Pfam; PF01558; POR, N; 1.

Pfam; PF01855; POR, N; 1.

Pfam; PF01855; POR, N; 1.

PFAM; PF01855; POR, N; 1.

PRINTS; PR00369; FLAVODOXIN.

PRINTS; PR00371; FPNCR.

PROSITE; PS00198; 4FE45_PERREDOXIN; 2.

PROSITE; PS00201; PLAVODOXIN LIKE; 1.

PROSITE; PS50902; PLAVODOXIN LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:000000; P:pyruvate metabolism; IS
InterPro; IPR001450; 4Fe45; ferredoxin.
InterPro; IPR003097; FAD binding.
InterPro; IPR003097; FAD binding.
InterPro; IPR0010954; Flav nitox synth.
InterPro; IPR001094; Flavdoxin like.
InterPro; IPR001094; Flavdoxin like.
InterPro; IPR001079; FFN cyt redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
InterPro; IPR002880; POR N.
InterPro; IPR009014; Transketo_C_like.
Pfam; PF00667; FAD binding_l; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send
                                                                                                                                                            YBS1 SCHPO STANDARD;
059681; O9USX5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update
Hypothetical protein Cl8E5.01 in chromosome
SPBC18E5.01 OR SPBC2983.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
NP_BIND
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METAL
METAL
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DOMAIN
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METAL
                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                      SCHPO
         MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bown Brooks K., Brown D., Brown S., Chillingworth T., Churches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt Electron}
                                                                                                   NCBI_TaxID=4896;
                                                                               SEQUENCE FROM N.A.
                                                                                                                       Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0045333; P:cellular respiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0016491; F:oxidoreductase activity;
                                                                                                                                                                                                                                                                                                                            492
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                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an
                                                                                                                                                                                                                                                                                                                                                  2 IPHPTNIHKYLVCESVNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pyrophosphate; Iron;
719 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transport; Oxidoreductase; Flavoprotein; NADP; FAD; FMN
                                                                                                                                                                                                                                                                                                                          VHHPSYVHKFDVLENIKQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                  719
722
725
729
729
776
7782
786
1288
1582
1583
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729
729
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779
782
786
1438
1553
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36.8%;
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IRON-SULFUR 1 (4FE-4S)
IRON-SULFUR 1 (4FE-4S)
IRON-SULFUR 1 (4FE-4S)
IRON-SULFUR 2 (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB Pred. No. 42; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               9
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(FLAVIN PART)
                                                                                                                                                                                                   update)
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42;
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LRT) (BY SIMILARITY)

BB3D60 CRC64;
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               D., Bowman
Churcher C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
                                        Stewart
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RESULT 11
CHI3_DROME
ID CHI3 ""
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RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Ocliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Ocliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Vonstreels E., Rieger M., Schaefer M., Whitehead S.,
RA Woodward J., Vonstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wabbutt R., Purnelle B.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.E., Paulsen I., Potashkin J.,
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880(2002).
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Best Local
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CHI3 DROME

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STANDARD

COUT-2003 (Rel. 42, Created)

COUT-2003 (Rel. 42, Last sequence up

15-MAR-2004 (Rel. 43, Last annotation

Label annotation

Coupling the coupling of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the cycloisomerase 2 family.
                    MEDLINE=22426071; PubMed=12537574;
Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin "Karpen G.H.;
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein DOMAIN 163 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL022299; CAA18396.1; -.
Yasuhara J.C., Wa
Karpen G.H.;
"Heterochromatic
                                                                                                                                                                                                                                              Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T40090; T40090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPombe; SPBC18E5.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAA22661.1;
     sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.6%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                    (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-VAL.
MW; AE39A39B053F704F CRC64;
     in
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Pred. No. 7.
  a Drosophila whole-genome shotgun
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8
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RESULT 12
CHIT_BRUMA
ID CHIT_B
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Best Local S
Matches 7
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Pfam; PF00704; Glyco_hydro_18; 1.

ProDom; PD000471; Glyco_hydro_18; 1.

SMART; SM00494; CCHEDD; 2.

SMART; SM00636; Glyco_18; 1.

PROSITE; PS50940; CHIT_BIND_II; 2.

PROSITE; PS50940; CHIT_NASE_18; FALSE_NEG.

PROSITE; PS01095; CHITINASE_18; FALSE_NEG.

PROSITE; PS01095; CHITINASE_18; PALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update
Endochitinase precursor (EC 3.2.1.14) (MF1
Brugia malayi (Filarial nematode worm).
Eukaryota; Metazoa; Nematoda; Chromadorea;
Onchoercidae; Brugia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multigene
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0022701; Cht3.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages acetyl-D-glucosamine polymers of chitin.
-!- SIMILARITY: Belongs to chitinase class II (family 18 of
                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDILINE=92179220; PubMed=1542646; Fuhrman J.A., Lane W.S., Smith R.F., Piessen "Transmission-blocking antibodies recognize in brugian lymphatic filariasis."; Proc. Natl. Acad. Sci. U.S.A. 89:1548-1552.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF026502; AAB81860.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98324849; PubMed=9662472; de la Vega H., Specht C.A., Liu Y
                                                                                                                                                                                             NCBI_TaxID=6279;
                                                                                                                                                                                                                                                                                                                                                                              P29030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 2 chitin-binding type-2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila.";
Insect Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Chitinases are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Genome Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                           FUNCTION: Microfilarial
                                                                                                                                                                                                                                                                                                                                                                                                   BRUMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPHPTNIHKYLVC
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295
458 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Specht C.A., Liu Y., e a multi-gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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bred. No.
      chitinase, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 13;
2; Mismatches
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CHITIN-BINDING TYPE-2 2.
PROTON DONOR (BY SIMILARITY).
4A063190B7E96248 CRC64;
    89:1548-1552(1992).
hitinase, which may function
res in the micro-filaria or i
                                                                                          R.F., Piessens W.F., Perlei
ies recognize microfilarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in Aedes,
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(MF1 an
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                                                                                                                                                                                                                                                Spirurida;
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                                                                                                                Perler
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into
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RS10_FUSNN
ID RS10_FUS
AC QBRIF4;
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Best Local S
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ACT_SITE
SEQUENCE
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DOMAIN
DOMAIN
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PIR; A
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PHPTDCHLFIQC PHPTNIHKYLVC 14

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Similarity
6; Conserv

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55971

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CHITIN-BINDING PROTON DONOR (E A78BE7BFB8E3709B

YB)

SIMILARITY)

TANDEM

Conservative

39.1%;

Score 45; DB Pred. No. 14; 3; Mismatches

1;

Length 504

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Gaps

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Pram; PF01607; CBM 14; 1.

Pram; PF00704; Glyco hydro 18; 1.

ProDom; PD000471; Glyco hydro 18; 1.

SMART; SM00494; ChtBD; 1.

SMART; SM00636; Glyco 18; 1.

SMART; PS0940; CHIT BIND II; 1.

PROSITE; PS01095; CHITINASE 18; 1.

Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Antigen; Repeat; Glycoprotein; Calcium-binding.

SIGNAL 22

FRINCHITH STORY AND ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a continued the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002557; Chitin bind_PerA.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 chitin-binding type-2
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23
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401
407
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400
448
448
504
CATALYTIC.

CATALYTIC.

SER/THR-RICH (LINKER).

3 X 14 AA APPROXIMATE T

3 X 14 BINDING TYPE-2.
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linkages of N-
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L outstation -
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28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 2586;
MEDLINE=21886394; PubMed=11889109;
             Bhattacharyya A., Bartman
Vasieva O., Chu L., Kogan
Larsen N., D'Souza M., Wal
Fonstein M., Kyrpides N.,
                                                                                                                                                                                                              RPSJ OR FN1646.
                                                                          Kapatral V., Anderson
                                                                                                                                                                                                Fusobacterium
                                                                                                                                                NCBI_TaxID=76856;
                                                                                                                                                                             Fusobacterium nucleatum (subsp. nucleatus;
Bacteria; Fusobacteria; Fusobacterales;
                                                                                                                                                                                                                              ribosomal
                                                                                                                                                                                                                                                                                                       FUSNN
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3 (Rel. 41, Last sequence upd:

)3 (Rel. 41, Last annotation u
                                                                                                                                                                                                                                                                                                       STANDARD;
Extman A., Gardner W., Grechkin G., & Kogan Y., Chaga O., Goltsman E., Ber ., Walunas T., Pusch G., Haselkorn R. & N., Overbeek R.;
                                                                                                                                                                                                                                                                                                        103
                                                                                                                                                                                                                                            update)
                                                                                                                                                                                    Fusobacteriaceae;
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                    in G., Zhu L
Bernal A
                                                                            Lykidis
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RESULT 15
VSP1_AGKCO
ID VSP1_A
AC P09872
DT 01-MAR
DT 01-FEB
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E1A_ADEC2
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Matches
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InterPro; IPR001848; Ribosomal_S10.

InterPro; IPR005731; Ribosomal_S10_b.

R Pfam; PF00338; Ribosomal_S10; 1.

R PRINTS; PR00971; RIBOSOMALS10.

R PTODom; PD001272; Ribosomal_S10; 1.

PTODOM; PD001272; Ribosomal_S10; 1.

R TIGREAMS; TIGR01049; TPSU_bact; 1.

R PROSITE; PS00361; RIBOSOMAL_S10; 1.

R PROSITE; PS00361; RIBOSOMAL_S10; 1.

SEQUENCE 103 AA; 11541 MW; EP5AA895BBF63DCA CRC64;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
  VSP1 AGKCO
P09872;
01-MAR-1989
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P35981;
01-JUN-1994
01-JUN-1994
01-JUN-1994
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J. Bacteriol. 184:2005-2018(2002).
-I- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=90163565; PubMed=2623943;
Spibey N., McClory R.S., Cavanagh H.M.A.;
"Identification and nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Early E1A 20 kDa protein.
Canine adenovirus type 2.
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             canine adenovirus types 1 and 2."; Virus Res. 14:241-256(1989).
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-!- SIMILARITY: Belongs to the S10P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; SEQUENCE 171 AA; 18942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; B60010; B60010.
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9; Conserv
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     10, Created)
28, Last seq
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52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                     Early protein.
MW; 2527EC1338062FB0 CRC64;
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     sequence
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Pred. No. 6.2;
4; Mismatches
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InterPro; IPR001254; Peptidase S:
InterPro; IPR001314; Peptidase S:
InterPro; IPR001314; Peptidase S:
Pfam; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPC; 1.
PR0SITE; PS02040; TRYPSIN_DM; 1.
PR0SITE; PS02134; TRYPSIN_HIS; PP
PR0SITE; PS0134; TRYPSIN_SER; 1.
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Viperidae; Crotalinae; Agkistrodon.
NCBI_TaxID=8713;
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Ancrod (EC 3.4.21.74) (Venombin A) (Protein C activator
Agkistrodon contortrix contortrix (Southern copperhead)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, But
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kisiel W., Kondo S., Smith K.J., "Characterization of a protein C contortrix contortrix venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87308291; PubMed=3624272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McMullen B.A., Fujikawa K., Kisiel W.; "Primary structure of a protein C activator from contortrix contortrix venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89229065; PubMed=2653426; McMullen B.A., Fujikawa K., Kisiel
                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 28:674-679(1989).
                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.178;
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FUNCTION: Thrombin-like snake venom serine protease. Cle
fibrinopeptides AM, AO, and AY, the aberrant fibrinogen
incapable of being cross-linked, forming easily dispersi
 134
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Agkistrodon
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Search completed: March Job time: 2.76709 secs

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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9u6r7 dermatophag
QBmnx4 caenorhabdi
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Q9s792 nicotiana t
Q9xfj4 nicotiana t
Q9xfj4 nicotiana t
Q9xfj4 drosophila
Q9vst9 drosophila
Q9vsu2 drosophila
Q9vsu2 drosophila
Q9vsu2 drosophila
Q9vx1 agkistrodon
Q4079 anopheles g
Q211139 caenorhabdi
Q7t229 bothrops ja
Q94de8 oryza sativ
Q9vr79 drosophila
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Query Match 94.8%; Score 109; DB 5; Length 555; Best Local Similarity 95.0%; Pred. No. 1.4e-09; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	GIYCOSIGASE; AYGIOLASE. SEQUENCE 555 AA; 63238 MW; 0E4564A1A459B30B CRC64;	PROSITE; PS01095; CHITINASE_18; 1.		SMART; SM00494; ChtBD2; 1.	ProDom; PD000471; Glyco_hydro_18; 1.	Pfam; PF00704; Glyco_hydro_18; 1.	InterPro; IPR001579; Glyco_hydro_18AS.		InterPro; IPR002557; Chitin bind PerA.	GO:0006030; P:chitin metabolism; IEA.	GO:0005975; P:carbohydrate metabolism; IEA.	GO:0016798;	GO:0008061;	GO; GO:0005576; C:extracellular; IEA.	EMBL; AF178772; AAD52672.1;	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.		on of a 98 kDa	Weber E.R., Hunter S., Stedman K., McCall C.;	QUENCE FROM N.A.	[1]	NCBI TaxID=6954;	Pyroglyphidae; Dermatophagoides.	ptidia; Ana		Dermatophagoides farinae (House-dust mite).	llergen.	(TrEMBLrel. 25, Last annotation	μ.	01-MAY-0000 (TremBire] 13. Created)	Q906R7 PRELIMINARY; FRT; 555 AA.	1

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01-OCT-2002
01-JUN-2003
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O1-JAN-1998 (
O1-JAN-1998 (
O1-OCT-2003 (
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
WMEL; AF098996; AAM34815.1; ...
WormPep; T11F1.7; CE23978.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015006; F:epidermal growth factor receptor activ
InterPro; IPR000494; EGFR L domain.
Pfam; PF01030; Recep_L_domain; 2.
Hypothetical protein.
SEQUENCE 523 AA; 60198 MW; CODCF493F0C34ED5 CRC64;
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MEDLINE=99069613;
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Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                    Aedes aegypti (Yellowfever mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
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                       SEQUENCE FROM N.A.
MEDLINE=98324849; PubMed=9662472;
de la Vega H., Specht C.A., Liu Y.,
"Chitinases are a multi-gene family
                                                                                                                                                                                                                                                                                                                                                                                                                  017412
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Waterston R., Wamsley
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NCBI_TaxID=7159;
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Science 282:2012-2018(1998).
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itinase 2 (EC 3.2.1.14).
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Caenorhabditis.
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                       THE 1,4-BETA-LINKAGES CHITIN.
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GO: 0005576; C:extracellular; IEA.
GO; GO: 000861; F:chitin binding; IEA.
GO; GO: 0008843; F:endochitinase activity.
GO; GO: 0016798; F:hydrolase activity.
GO; GO: 0005975; P:carbohydrate metaboli
STRAIN=cv. XANTHI; TISSUE=Anther;
Liu Z.H., Xia M., Poovaiah B.W.;
"Chimeric calcium/calmodulin-dependent pr
"cobacco:differential regulation by calmod
plant Mol. Biol. 0:0-0(1998).
-!- SIMILARITY BELONGS TO THE SER/THR FA
EMBL; U38446; AAF21450.1; -
EMBL; U38446; AAF21450.1; -
EMBL; AF087813; AAD52092.1; -
EMBL; Q63450; 1A06.
GO; GO:0005524; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
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Pfam; PF00704; Glyco hydro 18; 3.

Probom; PD0000471; Glyco hydro 18; 3.

Probom; SM00494; ChtBD2; 3.

SMART; SM00636; Glyco 18; 3.

PROSITE; P801095; CHITINASE 18; 3.
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Q9S792;
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InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18A8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
lamiids; Solanales; Solanaceae; Nicoting
NCBI Tayto-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium/calmodulin dependent CCAMK OR CCAMK-1.
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                                                                                                                                                                                                                                                                                "Regulated expression of an anther-specific calcium/calmodulin dependent protein kinase causes male sterility in plant."; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. XANTHI;
Liu Z., Poovaiah B
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotiana tabacum (Common Eukaryota; Viridiplantae;
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GO:0008061; F:chitin binding; IEA.
GO:0008043; F:enditin binding; IEA.
GO:0008043; F:hydrolase activity, acting on
GO:0005975; F:carbohydrate metabolism; IEA.
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Liu Z.H., Xia M., Poovaiah B.W.;

I'll "Chimeric calcium/calmodulin-dependent protein kinase in tobacc differential regulation by calmodulin isoforms.";

I'll differential regulation by calmodulin isoforms.";

LL Plant Mol. Biol. 0:0-0(1998).

-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASE EMBL; AF145593; AAD28791.1; -.

REMBL; AF145592; AAD28791.1; -.

REMBL; U70922; AAD28098.1; -.

REMBL; O63450; IAO6.

REMSCP; O63450; IAO6.

REMSCP; O63450; F:calcium ion binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

REMO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

REMO; GO:0016740; F:transferase activity; IEA.

REMO; GO:0016740; F:transferase activity; IEA.

REMO; GO:0006468; P:protein amino acid phosphorylation; IEA.

REMO; INTERPO; IPR000719; Prot kinase.

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R ProDom; PD000012; EF-hand; 1.

R ProDom; PD0000012; EF-hand; 1.

R PRODom; PD0000014; EF-hand; 1.

R SMART; SM00054; EFh; 3.

R SMART; SM00250; S TKc; 1.

R PROSITE; PS00018; EF-HAND; 3.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00110; PROTEIN KINASE DOM; 1.

R PROSITE; PS00110; PROTEIN KINASE ST; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

SEQUENCE 517 AA; 57624 MW; BB6706E29AFB349D CRC64;
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GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016746; P:protein amino acid phosphorylation;
InterPro; IPR002048; ZF-hand.
InterPro; IPR001719; Prot_kinase.
InterPro; IPR001715; Recoverin.
InterPro; IPR001290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002291; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008671; Ser_thr_pkinase.
InterPro; I
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINSCV. XANTHI; TISSUE-Anther;
Wang W., Liu Z.H., Xia M., Poovaiah B.W.;
Wang Calcium/calmodulin-dependent protein kinase in
differential regulation by calmodulin isoforms,";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
Iamidds; Solanales; Solanaceae; Nicotiana.
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Eukaryota; Viridiplantae; Streptop
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nilarity 58.8%;
Conservative
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Pred. No. 1.4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517
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ID Q9VST9
AC Q9
DT 000

Q9VST9 Q9VST9; 01-MAY-2000 (TrE 01-OCT-2002 (TrE 01-OCT-2003 (TrE CG4821 protein.

(TrEMBLrel. 13, 2 (TrEMBLrel. 22, 3 (TrEMBLrel. 25,

Last sequence update)
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PRELIMINARY;

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RESULTATION OF THE PROPERTY OF
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RESULT 7
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Best Local S
Matches 8
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Best Local S
Matches 10
                                                                                                                                                                                                                                         FIGURE 437 AA, 49481 MW, 1D2D73B1E725,
FIGURE 437 AA, 49481 MW, 1D2D73B1E725,
FIGURE 437 AA, 49481 MW, 1D2D73B1E725,
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Q8T015;
01-JUN-2002
01-JUN-2002
01-CCT-2003
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ProDom; PD000012; EF-hand; 1.

ProDom; PD0000012; Prot_kinase; 1.

SVART; SM00054; EFh; 3.

SMART; SM00220; S_TKC; 1.

SROSITE; PS00018; EF HAND; 3.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS500108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

AND-binding; Kinase; Serine/threonine-protein kinase; 7

AND-binding; Kinase; S7881 MW; 48F8361E2E80AE61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa'Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEQUILA OR CG4821 OR CG4948 OR CG18403.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00036; Pfam; PF00069;
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8; Conserv
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                                                                   PHPHDVHKYLRC 109
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                                                                                                                                                            Conservative
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66.7%;
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(Fruit fly).
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25,
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                                                                                                                                                       Score 54; DB:
Pred. No. 1.7;
2; Mismatches
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1.7;
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os bresphila on Cos491 on Cos494 on Col4403.

os bresphila melanogaster (Fruit Fly)

oc bukaryota; Metanoz; Arthropoda; Hesapoda; Insecta; Pterygota;

oc bephers; Endepresygota; Dipeera; Springer, Muscomorpha;

prophydiodea; Prosphilides; Drosphila.

RC STRAIN-Beptaloy;

RM MEDINE-2019506; L. Levis S. S., Lil P. M. Bookins R.A. Gocayne J.D.,

RA Admantides; P.G., Scherer S.J. Lil P.M. Bookins R.A. Golle R.F.,

RA George R.A. Levis S.S., Richards S., Abburner M., Renderson S.M.,

RA Admantides; P.G., Scherer S.J., Lil P.M. Bookins R.A. Golle R.F.,

RA George R.A. Levis S.S., Richards S., Abburner M., Renderson S.M.,

RA Bandun R.D. Ostrman J.R., Mandell M.D., Zhang G., McBrill, R.B.,

RA Bernder R.C., Dortman J.R., Yandell M.D., Zhang G., McBrill, R.B.,

RA Bernder R.C., Dortman J.R., Mandell M.D., Zhang G., McBrill, R.B.,

RA Bernder R.C., Berns P.V., Bernan B.F., Bhandari D., Bolshakov S.,

RA Berling R.M., Baru A., Beller H., Caddeu E., Center A., Chandra I.,

RA Berling R.L., Harry D., Heiman T.J., Hernander J.R., Bouck J.,

RA Harris N.L., Harry D., Heiman T.J., Hernander J.R., Hernander J.R.,

RA Harris N.L., Harry D., Heiman T.J., Hernander J.R., Hernander J.R.,

RA Harris N.L., Harry D., Heiman T.J., Hernander J.R., Hernander J.R.,

RA Harris N.L., Harry D., Heiman T.J., Hernander J.R., Wolkladon L.,

RA Harris N., May M., Marbi, B., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,

RA Harris N., Helson K.A., Bowland T.J., Wai M.-H., Ingewe C.,

RA Harris N., Helson K.A., March M., Borketten D., Harris M.

RA Harris N., Helson K.A., March M., Borketten J., Helson D.L.,

RA Harris N., May M., Marbi, B., Rather R., Dolfard J., Wai M.-H., Booke M.G.,

RA Harris N., May M., Marbi, B., Parksen R.D.C., Scheeler F., Wellson D.L.,

RA Harris N., March M., Marki, M., Marbi, M
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FlyBase; reywords; Go; Go:0005576; C:extracellular; lbn.
Go; Go:0005576; C:emembrane; IEA.
Go; Go:0016020; C:membrane; IEA.
Go; Go:0004061; F:chitin binding; IEA.
Go; Go:0004263; F:chymotrypsin activity; IEA.
Go; Go:0005044; F:scavenger receptor activity; IEA.
Go; Go:0005044; F:scavenger receptor activity; IEA.
Go; Go:0006295; F:trypsin activity; IEA.
Go; Go:0006295; P:trypsin activity; IEA.
Go; Go:0006295; P:trypsin activity; IEA.
Go; Go:0006508; P:proteolysis and peptidolysis; IEP
InterPro; IPR002557; Chitin bind_PerA.
InterPro; IPR002557; Chitin_bind_PerA.
InterPro; IPR001754; Peptidase_S1.
InterPro; IPR001154; Peptidase_S1A.
InterPro; IPR001190; Srcr_receptor.
R Pfam; PF01607; CBM 14; 15.
R Pfam; PF00057; Idl_recept_a; 2.
R Pfam; PF00057; Idl_recept_a; 2.
R Pfam; PF00057; Idl_recept_a; 2.
R Pfam; PF00050; SRCR; 2.
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GO; GO:00
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Pfam; PF01607; CBM 14; 7.
SMART; SM00494; ChEBD2: 7.
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Capovilla M., Lagueux M.;
Capovilla Persophila gene coding
"Graal a Drosophila gene coding
Submitted (MAR-2001) to the EMBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I SIMILARITY: BELONGS TO PEPTIDASE EMBL, AJ309005; CAC35209.1; -. TJ9Base: Bornovicki Particularity (Particularity Particularity Particularity
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Beobera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRAAL2 protein precursor. TEQUILA OR GRAAL OR CG4821
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chittn binding; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
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D., Celniker
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on of Drosophila melanogaster genome
(MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAR-2000)
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e EMBL/GenBank/DDBJ
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Bacu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Bouck J., Boukstein P., Brottlier P.,
RA Borkova D., Botchan M.R., Bouck J., Bouckstein P., Brottlier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Chamson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Hatwey D., Hesmand T.J., Hernandez J.R., Houck J.,
RA Harke N., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Hostin D., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu K., Matson K.A., Howland T.J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Hostin D.R., Pacleb J.M.,
RA Palazzolo M., Pithan G.S., Pan S., Pollard J., Puri V., Reese
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Best Local
Matches
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PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR00261; LDLRECTROTTR.
SMART; SM00494; ChtBD2; 15.
SMART; SM00192; LDLA; 2.
SMART; SM00192; LDLA; 2.
SMART; SM00202; Tryp_SPC; 1.
PR051TE; PS01209; LDLAA_1; 1.
PROSITE; PS00668; LDLRA_2; 2.
PROSITE; PS00668; LDLRA_2; 2.
PROSITE; PS00420; SRCR_1; 2.
PROSITE; PS00420; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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Q9VSU2; Q9VS
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01-OCT-2002
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TEQUILA OR CG4821 OR CG4948 OR
Drosophila melanogaster (Fruit
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-2000 (TrEMBLrel. 13, C
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Drosophila.
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Pred. No. 10;
2; Mismatches
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Doreett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriara S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Williams R.A., Kruse D., Li P., Mattei B., Moshrefi A.,

A Gonzalez M., Williams D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Nor, Park S., Patel S., Peiffer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Stapleton M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

"Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                       submitted (SEP-2002) to the EMBL/GenBank/DDBJ dat
-1- SIMILARITY: BELONGS TO PEPFIDASE FAMILY S1.
EMBL; AEGO355; AAF50319.3; -.
HSSP; P00755; IRTF.
FlyBase; FB9n0023479; Tequilla.
G0:00016020; C:membrane; IEA.
G0:G0:0016020; C:membrane; IEA.
G0:G0:0008524; F:ATP binding; IEA.
G0:G0:0008524; F:Chitin binding; IEA.
G0:G0:0008061; F:Chitin binding; IEA.
G0:G0:0004263; F:Chymotrypsin activity; IEA.
G0:G0:0004263; F:Scavenger receptor activity; IEA.
G0:G0:0006030; P:Chitin metabolism; IEA.
G0:G0:0006030; P:Droteolysis and peptidolysis; I
G0:G0:0015992; P:proteolysis and peptidolysis; I
                 InterPro; IPR000194; ATPase a/bcentre.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR002172; LDL_receptor A.
InterPro; IPR001724; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR00130; Sror receptor.
Pfam; PF00607; CBM 14; 15.
Pfam; PF00530; SRCR; 2.
Pfam; PF00530; SRCR; 2.
Pfam; PF00089; trypsin; 1.
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Submitted
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Celniker S.E., Adams
Evans C.A., Gocayne
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M.D., Celniker
ed (MAR-2000)
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              ; ldl_recept_a; 2.
; SRCR; 2.
; trypsin; 1.
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H., Wang X.,
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CHYMOTRYPSIN

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RESULT 11
QBUVX1
ID QBUVY
AC QBUVY
DT 01-M
DT 01-M
DT 01-C
DT 11-C
DT 
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Best Local S
Matches
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Best Local S
Matches 8
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SMART; SM00192; LDLA; 2.

SMART; SM00202; SR; 2.

SMART; SM00202; Tryp SPc; 1.

PROSITE; PS00152; ATPASE ALPHA BETA; 1.

PROSITE; PS01209; LDLA; 1; 1.

PROSITE; PS01209; LDLA; 1; 1.

PROSITE; PS00420; SRCR 1; 2.

PROSITE; PS00420; SRCR 2; 2.

PROSITE; PS50287; SRCR 2; 2.

PROSITE; PS50240; TRYPSIN DM; 1.

PROSITE; PS00134; TRYPSIN BER; 1.

PROSITE; PS00135; TRYPSIN BER; 1.
            QBUVX1 PRELIMINARY; PI
QBUVX1;
QBUVX1;
O1-MAR-2002 (TrEMBLrel. 20, Cre:
O1-MAR-2002 (TrEMBLrel. 25, Las:
O1-CCT-2003 (TrEMBLrel. 25, Las:
Thrombin-like serine protease ('
(EC 3.4.21.7).
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01-JUL-1997
01-JUL-1997
01-JUCT-2002
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MEDLINE=97225795; PubMed=9073065;

Modaira K.I., Oki M., Kakikawa M.,
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EMBL; X90510;
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Viruses; dsDNA viruses,
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SEQUENCE
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PR00258;
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8; Conser
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2786 AA;
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50.0%;
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22,
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se (Thrombin-like enzyme
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MW; 2EED7A7DA5002C76 CRC64;
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2; Mismatches
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Matches 10
                                                                                              Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PROSITE; PS00134; TRYPSIN HIS; 1

PROSITE; PS00134; TRYPSIN SER; 1

PROSITE; PS00135; TRYPSIN SER; 1

Hydrolase; Protease; Serine proteseQUENCE 260 AA; 28530 MM; 0
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GO; GO: 0008233;
GO; GO: 0004283;
GO; GO: 0004295;
GO; GO: 0006508;
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                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO PEPTIDASE EMBL; AF336126; AAL68708.1; -. EMBL; AF370124; AAM46086.1; -.
                                                                                                                                                                                GG; GO:0006508; P:proteolysis and pep
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase SiA.
InterPro; IPR001314; Peptidase_SiA.
                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2001) to
                                                                                                                                                                                                                                                                                                                                              "cDNA sequence analysis thrombin-like enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                            Agkistrodon ussuriensis. Submitted (JAN-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao Y., Fang K., Sun K.
"cDNA for thrombin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom gland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=35671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis)
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleost
                                                                                                                                                                                                                                SP; P00761; 1AN1.
GO:0004263; F:chymotrypsin activity; IGO:0004233; F:peptidase activity; IEA.
GO:0004283; F:plasmin activity; IEA.
GO:0004295; F:trypsin activity; IEA.
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                                                           Similarity
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                       DIPHPTNIH--KYLVCESVNGG
DVPHCANINILDYEVCQAAHGG
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Pred. No.
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                                                                                                 00514BE487B6F84C CRC64;
  182
                       20
                                                  Mismatches
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                                                                       Length
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O4407 DT 01-JU DT 01-Shen Z., Jacobs Lorena M.;

"Characterization of a novel gut-specific ch human malaria vector Anopheles gambiae.";

J. Biol. Chem. 272:28895-28900(1997).

EMBL; AF008575; AAB87764.1; -.

PIR; T44445; T44445.

GO; GO:0005576; C:extracellular; IEA.
GO; GO:000578; F:chttin binding; IEA.
GO; GO:0016798; F:hydrolase activity, acting 044079; 01-JUN-1998 Eukaryota; Neoptera; E 01-JUN-1998 01-OCT-2003 Anopheles gambiae (African malaria mosquito). AGCHI-1. 044079 MEDLINE=98030563; PubMed=9360958; TISSUE-Gut; SEQUENCE FROM N.A. ; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Endopterygota; Diptera; Nematocera; Culicoidea; Ano (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. PRELIMINARY; 25, Last sequence update)
Last annotation updat Created) PRT; 525 acting A chitinase update) g glycosyl gene

Anopheles

bonds;

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Q21139
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Best Local S
Matches 9
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                         Waterston R.;
Waterston R.;
Submitted (MAY-2003) to the EM Submitted (MAY-2003) to the EM EMBL; U40942; AAC47074.5; -
PIR; T16525; T16525.
PIR; T16525; T16525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005975; P:carbohydrate metabolism; IE
GO; GO:0006030; P:chitin metabolism; IEA.
InterPro; IPR002557; Chitin bind perA.
InterPro; IPR001579; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18AS.
Pfam; PP00704; Glyco hydro 18; 1.
Pfam; PP00704; Glyco hydro 18; 1.
ProDom; PD000471; Glyco hydro 18; 1.
SMART; SM00656; Glyco 18; 1.
SMART; SM00656; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
Glycosidase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Wu X., Leimbach D.;
"The sequence of C. e
Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                  WormPep; K02E10.8; CE3
InterPro; IPR003599; I
InterPro; IPR007110; I
InterPro; IPR003598; I
                                                                                                                                                            Pfam; PF00047; 19; 4. SMART; SM00409; IG; 4. SMART; SM00408; IGC2; 4. PROSITE; PS50835; IG_LIKE; 5. SEQUENCE 727 AA; 80863 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01.-VUV-1996 (TrEMBLrel. 01, Create 01.-JUN-2003 (TrEMBLrel. 24, Last s 01-OCT-2003 (TrEMBLrel. 25, Last a Synaptogenesis abnormal protein 1. K02E10.8 OR SYG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q21139
Q21139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOZEIO.8 OR SYG-1.
Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycosidase;
SEQUENCE 5:
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                                                                          Similarity 9; Conserv
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  IPHPTNIHKYLVCES 16
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                                                                            Conservative
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Ig-like.
Ig_c2.
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                                                                        Score 52; DB
Pred. No. 6.3;
2; Mismatches
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                                                                                                                                                                 C623B14C92205E2A CRC64;
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                                                                                                                   Length 727;
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D Q94DE8

D Q94DE8

C Q94DE8;

O (1-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 25, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 25, Last annotation update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE P0633F02.4 protein (OJ1402H07.12 protein).

GN P0633F02.4 OR OJ1402H07.12.

OS Oryza sativa (Rice), and

OS Oryza sativa (Ri
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Best Local (
Gramene; Q94DE8; -. Gramene; Q94DE8; -. G0; G0:0005622; C:intracellular; I) G0; G0:0003725; F:double-stranded InterPro; IPR001064; Crystallin. TnterPro; IPR001159; DS_RBD.
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Q7T229;
                                                                                                                                                                              EMBL; AP003289; BAB63701.1; EMBL; AP003415; BAC03323.1;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SPECIES=0.sativa (japonica cultivar-group);
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, clone:P0683F02.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=O.sativa; STRAIN=cv. Nipponbare; Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kashima S., Roberto P.G., Soares A.M., Astolfi-Filho S., Giglio J.R., Franca S.C.; "Analysis of Bothrops jararacussu venomous gland transcr structural and functional categories: gene expression prhighly expressed phospholipases A2."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bothrops jararacussu (Jararacussu).

Bukaryota; Metazoa; Chordata; Craniatz
Lepidosauria; Squamata; Scleroglossa;

Viperidae; Crotalinae; Bothrops.

NCBI_TaxID=8726;
                                                                                                                                                                                                                                             Submitted (MAR-2001) to the
                                                                                                                                                                                                                                                                                clone:OJ1402_H07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                      'Oryza sativa nipponbare (GA3)
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DR PROSITE; P800225; CRYSTALLIN_BETAGAMMA; 1.

DR PROSITE; P850137; DS_RBD; 1.

SQ SEQUENCE 721 AA; 80021 MW; 6A004326F07646DA CRC64;

Query Match

Best Local Similarity 44.3%; Score 51; DB 10; Length 721;

Best Local Similarity 44.4%; Pred. No. 9.2;

Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIPHPTNIHKYLVCESVN 18

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Db 436 DIPYAPDVGDYLVCESUN 453

Search completed: March 22, 2004, 06:59:11

Job time: 7.02446 secs
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Result
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## ALIGNMENTS

Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fel canine; veterinary; antibody; vaccine; immunisation. 17-APR-1998; 13-MAY-1998; 22-FEB-2000 02-SEP-1998; 28-OCT-1999. Dermatophagoides farinae. AAY52512 standard; peptide; 20 16-APR-1999; WO9954349-A2 House dust mite allergen protein (map) (HESK-) HESKA CORP. (first entry) 98US-00062013. 98US-0085295P. 98US-0098909P. 99WO-US008524. A A/B fragment map(2) diagnosis; human; feline;

Claim 3; Page 69; 154pp; English.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

WPI; 2000-052700/04.

Mccall CA,

Hunter SW,

Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWM nmap) composition. The HMM-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. The HMM-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines,

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RESULT 2
AAU96316
Query Match
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                                                                          The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus
                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
                              reducing hypersensitivity responses to mite allergens, and as vacciagainst mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                           Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mccall CA,
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                                                                                                                                                                                                                                                                                                                                          mite allergenic protein isolated from Dermatophagoides, HMW-map protein, useful as a vaccine for treating mite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIPHPTNIHKYLVCESVNGG
                                                                                                                                                                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hunter SW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           American house dust mite; antiallergic; mite; IgE; nic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                        70; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           farinae.
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                                                          nd to Der Hrwm-way uncomplex formation, thus to prevent immunocomplex formation, thus
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Pred. No. 7.1e-12;
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Query Match

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Matches Query Match

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DIPHPTNIHKYLVCESVNG 19

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RESULT 3
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13-MAY-1998;
02-SEP-1998;
                                              mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used a vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
                                                                                                                                                                                                                                                                                                                                                                  Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein -map) composition. The HMW-map composition was isolated from a D. fa homogenate by gel filtration, with each fraction being analysed for presence of proteins that bound to IgE present in mite-allergic dog antisera. The HMW-map composition comprises mapA (a 109 kD protein)
  Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-052700/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mite allergen protein; map; high molecular weight; HMW-man house dust mite; IgE; immunoglobulin E; allergen; mapA; muhypersensitivity reaction; therapy; treatment; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mite allergen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 70; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nove1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mccall CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             canine; veterinary; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HESK-) HESKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                high molecular weight
to modify an animals' h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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  AA;
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98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dermatophagoides nucleic acid ponypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/B fragment map(10)
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMW-map; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mapB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; feline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein (HWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               D. farinae
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RESULT 5
AAY52525
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AC AAY5
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AC AAY5
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DT 22-F
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AAU96324
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                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for ellciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-protein acceptable to or having an allergic response to a mite. A protein susceptible to or having an allergic response to a mite. A protein can be used in the callergic response to a mite. The DNA and protein can be used in the callergic response to a mite. The DNA and protein can be used in the callergic response to a mite. The DNA and protein can be used in the callergic response to a mite. The DNA and protein can be used in the callergic response to a mite. The DNA and protein can be used in the callergic response to a mite of the invention of immunoglobulin (19% or Der HMW-map protein activity associated with a callergen. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to 19%, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ABU96314-ABU96342 or represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                     Sequence 19
   House dust mite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mite allergenic protein
Der HMW-map protein, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-351888/38
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                                                                         AAY52525;
                                                                                                        AAY52525 standard; protein; 536
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                                     22-FEB-2000
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                                                                                                                                                                                                                             DIPHPTNIHKYLVCESVNG 19
                                                                                                                                                                                              DIPHPTNIHKYLVCESVNG
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                                                                                                                                                                                                                                                               94.8%; Score 109; DB 5; larity 100.0%; Pred. No. 6.7e-11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-00662293
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                                     (first entry)
   ê.
   farinae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated from Dermatophagoides, as a vaccine for treating mite;
mite allergen protein (map) PDerf98-536
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RESULT 6
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AC ACU
DT 15-0
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DT 15-0
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XW Der
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15-JUL-2002

(first entry)

AAU96329 standard;

protein;

mite allergenic protein; immunocomplex formation.

Der HMW-map polypeptide #16

Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;

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Query Match
Best Local S
Matches 19
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13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                       allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
                                                                                                                                                                                                                                                                                                                       This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-536, the mature form of PDerf98-555 (AAY52523). PDerf98-536 has a molecular weight of 98 kD, comprising 536 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to Ig3 present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite-allergic dog antisera.
                                                                                                                                           Sequence 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 125-127; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel high molecular weight used to modify an animals' h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ38579, AAZ38580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dermatophagoides farinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-052700/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9954349-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      canine; veterinary; antibody; vaccine; immunisation.
 493
                                                                    19;
                                 1 DIPHPTNIHKYLVCESVNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HESKA CORP
                                                                                       Similarity
 DIPHPTNIHKYLVCEFVNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hunter SW,
                                                                    Conservative
                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00062013.
98US-0085295P.
98US-0098909P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US008524
                                                                                     94.8%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                t Dermatophagoides nucleic acid po
hypersensitivy to mite allergens
                                                               Pred. No. 3.3e-09;
512
                                 20
                                                                                                    Length 536;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides
                                                                    0
                                                                    Gaps
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RESULT 7
AAY52523
ID AAY5
XX AAY5
AC AAY5
XX AAY5
XX AAY5
XX Mite
DE Hous
XX Mite
KW hous
XX hous
KW hous
XX hype
XW cani
XX hype
FT Pept
FT Prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)8 or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite who may an allergic response to a mite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New
                                                                                                                                            Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dermatophagoides
                                                                                                                                                                                                                                                            22-FEB-2000
                                                                                                                                                                                                                                                                                                                       AAY52523 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200222807-A2
                                                                                                                                                                                                                          House dust mite (D. farinae) mite allergen protein (map) PDerf98-555
                                  Protein
                                                                                                                Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HESK-) HESKA CORP
                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMW-map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mite allergenic protein isolated from Dermatophagoides, designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-351888/38
                                                                                                                                                                                                                                                                                                                                                                                                       493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIPHPTNIHKYLVCESVNGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       DIPHPTNIHKYLVCEFVNGG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 125-127; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                           (first entry)
                                                                               Location/Qualifiers
                     /note=
                                                note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               farinae.
                                                                                                                                                                                                                                                                                                                       protein;
                                   .
555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.8%;
                   "Mature PDerf98-555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber
                                                                                                                                                                                                                                                                                                                         555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 109; DB 5;
Pred. No. 3.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     器
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                    (map) PDerf98-555, PDerf98-555 has a molecular weight of 98 kD, comprising 555 amino acids, and is a component of the Dermatophagoides of farinae high molecular weight mite allergen protein (HWM-map) composition. The HMW-map composition was isolated from a D. farinae composition. The HMW-map composition was isolated from a D. farinae composition and protein and protein analysed for the presence of proteins that bound to 1gE present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an carimal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as
                                                                                    Query Match
Best Local :
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-052700/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1999
                                                                                                                                                                        allergens from a mixture of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 111-113; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9954349-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents Dermatophagoides farinae mite allergen protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HESK-) HESKA
 512
                            1 DIPHPTNIHKYLVCESVNGG
                                                                  l Similarity
19; Conserv
 DIPHPINIHKYLVCEFVNGG
                                                                                                                                       555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hunter SW,
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORP.
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98US-0085295P.
98US-0098909P.
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                                                                                    94.8%;
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                                                                  0,
                                                                                    Score 109;
Pred. No. 3
531
                                20
                                                                     Mismatches
                                                                                    DB 3;
.5e-09;
                                                                                                  Length 555;
                                                                   Indels
                                                                   0;
                                                                  Gaps
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RESULT 8
AAU9637
ID AAU9
XX AAU9
XX AAU9
XX Der
XX 1mmu
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                                                                                                                                    21-MAR-2002
                                                                                                                                                                                                                                                                        WO200222807-A2
                                                                                                                                                                                                                                                                                                                                                                                                      Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Der HMW-map; American house dust mite; antiallergic; mite; I mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; protein; 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide #14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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14-SEP-2001; 2001WO-US028730.

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Best Local
          WPI; 2002-351888/38.
N-PSDB; ABK69573.
                                                                                                     14-SEP-2000; 2000US-00662293
                                                                                                                               14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                    WO200222807-A2
                                                                                                                                                                                                             Dermatophagoides farinae
                                                                                                                                                                                                                                      Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                     15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map receive are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANU96314-ANU96342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mite allergenic protein isolated from Dermatophagoides, Der HMW-map protein, useful as a vaccine for treating mite
                                                                                                                                                                                                                                                                                           Der HMW-map polypeptide #15
                                                                                                                                                                                                                                                                                                                                                                        AAU96328 standard; protein; 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-351888/38.
                                                                              (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated mite allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                           512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Page 114-116; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           DIPHPTNIHKYLVCEFVNGG 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIPHPTNIHKYLVCESVNGG 20
                                                    Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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A
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95.0%;
                                                    Weber ER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 109; DB 5;
Pred. No. 3.5e-09;
); Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oides, designated mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its related nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 10
AAY52535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                      17-APR-1998;
13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                               Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy, treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog,
                                                          Mccall CA,
                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2003
22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY52535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                  16-APR-1999;
                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                    Dermatophagoides pteronyssinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY52535 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 120-122; 161pp; English.
                                                                                                                                                                                                                28-OCT-1999
                                                                                                                                                                                                                                              WO9954349-A2
                                                                                          HESK-) HESKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 DIPHPTNIHKYLVCEFVNGG 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                          Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first en
                                                                                          CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relates to an isolated mite allergenic protein of
                                                                                                                                      98US-00062013.
98US-0085295P.
                                                                                                                      98US-0098909P
                                                                                                                                                                                  99WO-US008524
                                                                                                                                                                                                                                                                                         240.
                                                                                                                                                                                                                                                                                                                        115. .117
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                       'note= "Asn is N-glycosylated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.8%;
95.0%;
                                                                                                                                                                                                                                                                         "Asn is N-glycosylated"
                                                            Weber ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109; DB 5; L
Pred. No. 3.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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WPI; 2000-052700/04. N-PSDB; AAZ38589, AAZ38590

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RESULT 11
AAU96339
##X#X555555555555555555555555555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AAYSSSSS). Nucleic acid molecules encoding Pherp98-490 were isolated from a D. pteronyssius cDNA library by hybridisation with a probe encoding the D. farinae high molecular weight map (HMW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's them, compositivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, cother pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            mite allergenic protein; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                     14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                                                                                                                       21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                         WO200222807-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Der HYM-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Der HMW-map polypeptide #26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU96339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU96339 standard;
                                                                                      New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                            WPI; 2002-351888/38.
N-PSDB; ABK69585.
                                                                                                                                                                                                                                                                   14-SEP-2000; 2000US-00662293
                                                                                                                                                                                              Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490 has a molecular weight of 98 kD, comprising 490 amino acids, and has a high degree of homology with the D. farinae mature 98 kD allergen, maps
                                                                                                                                                                                                                                  (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 IPHPINIHKYLVCESV---NGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 147-149;
                                                                                                                                                                                              Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154pp; English.
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic

This sequence protein (map)

represents Dermatophagoides pteronyssius PDerp98-509. PDerp98-509 has a molecular

mite allergen weight of 98 kD

Claim 12; Page 144-146; 161pp; English

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proteinaceous epitope is useful for identifying an animal (e.g., dog,
cat) susceptible to or having an allergic response to a mite. A
therapeutic composition is useful for desensitising a host animal to an
allergic response to a mite. The DNA and protein can be used in the
detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
disease. Antibodies that bind to Der HMW-map are useful for inhibiting
binding of proteins to IgE, to prevent immunocomplex formation, thus
reducing hypersensitivity responses to mite allerges, and as vaccines
against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                   17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mite allergen protein; map; high molecular weight; HYW-map; allergy; house dust mite; Igg; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-2003
22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 490 AA;
                                                                   Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D. pteronyssius
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY52533;
                                       Claim 3; Page 134-136; 154pp; English
                                                                                                               N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588
                                                                                                                              WPI; 2000-052700/04
                                                                                                                                                           Mccall
                                                                                                                                                                                                                                                                             16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                 Protein
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                                                                                                                                                                                       (HESK-) HESKA
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14; Conserv
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                                                                                                                                                           Hunter SW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
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98US-0085295P.
98US-0098909P.
                                                                                                                                                                                                                                                                             99WO-US008524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 kD mite allergen protein (map)
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   /note= "Mature PDerp98~509"
                                                                                                                                                                                                                                                                                                                                                                                             /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                    . 509
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                                                                                                                                                           Weber ER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 82.5; D
Pred. No. 7.5e
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDerp98-509
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RESULT 13
AAU96337
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
                                                                                                                                                                                                                                                                                                                 Claim 12; Page 134-136; 161pp; English.
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                                                                                           The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting brides.
                          disease. Antibodies that bind to Der HMM-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMM-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-351888/38.
N-PSDB; ABK69583.
                                                                                                                                                                                                                                                                                                                                                  New mite allergenic protein isolated from Dermatophagoides,
Der HMW-map protein, useful as a vaccine for treating mite a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mite allergenic protein; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WC200222807-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Der HMW-map; American house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Der HMW-map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                               Page 139-141; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide #25
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use dust mite; antiallergic; mite; I immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                  mite allergy
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RESULT 15
AA017674
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                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                              The present invention relates to isolated protein allergens from the Blomia tropicalis mitc, designated Blot 3 and Blot 12(8). The protein allergens are useful for preventing, reducing or ameliorating a B. tropicalis hypersensitivity condition, such as asthma, atopic dermatitis or rhinitis. The present sequence is a protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein allergens from the mite Blomia tropicalis, useful as vaccine for preventing, reducing or ameliorating a B. tropicalis hypersensitivity or allergic conditions, e.g. asthma, atopic dermatitis or rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mite; allergen; Blot 3; Blot 12(S); Blot 12; dust mite; immunisation; antiallergic; anti-inflammatory; immunomodulatory; storage mite; asthma; atopic dermatitis; rhinitis; gene therapy; vaccine.
                                                                                                                                                                                                                                                      Sequence 143 AA;
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N-PSDB; AAL46687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B tropicalis allergen variant Blot 12(S) protein SEQ ID NO: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAO17674 standard; protein; 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chua KY, Nge C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-2000; 2000AU-00000730.
13-OCT-2000; 2000AU-00000731.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 133; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYSI-) UNIV SINGAPORE NAT.
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100 IPHPGNVHKYIIC 112
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                                       2 IPHPTNIHKYLVC 14
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                                                                                                                            Conservative
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                                                                                                                      Score 67; DB 5; Length 143; Pred. No. 0.0067; Indels 3; Mismatches 1; Indels
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Search completed: March 22, 2004, 06:51:34
Job time: 8.08116 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
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115
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/cgn2_6/ptodata/2/pubpaa/US07_pUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
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score greater than or equal to the score of the result being and is derived by analysis of the total score distribution Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

## SUMMARIES

Result

Query

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seduetice sonsta,		Sequence 232599,	Sequence 274767,	Sequence 17, Appl	Sequence 260412,	Sequence 272856,	Sequence 5584, Ap	-	Sequence 35, Appl	Sequence 41, Appl	Sequence 18, Appl	æ	e 21	Sequence 11, Appl	Sequence 3, Appli	Description

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sequence 2 Sequence 1 Sequence 1 Sequence 5 Sequence 6 Sequence 7 Sequence 8 Sequence 8 Sequence 8 Sequence 8 Sequence 9 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2	equence 692 equence 27,

## ALIGNMENTS

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US-10-218-743-3
Sequence 3, Application US/10218743
Publication No. US20030096779A1
GENERAL IMFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: MOVEL DEBMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-03
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/59/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/98,565
PRIOR APPLICATION NUMBER: 60/98,565
PRIOR APPLICATION NUMBER: 60/98,565
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
PRIOR PRIOR DATE: 1998-04-17
PRIOR FILING DATE:
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US-10-218-743-3
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Best Local (
1 DIPHPTNIHKYLVCESVNGG
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Similarity 100.0%; Pred. No. 1e-10;
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                                                             SOFTWARE: Pat
SEQ ID NO 21
LENGTH: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/10218743
Publication No. US20030096779A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 11
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Best Local Similarity
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Publication No.
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                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/292,;
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
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CURRENT FILING DATE: 2002-08-13
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APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-05-13
ORGANISM: Dermatophagoides farinae 10-218-743-21
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                                                                                                                                      NUMBER OF SEQ ID NOS:
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                                                TYPE: PRT
                                                                                                                                                                         APPLICATION NUMBER: 09/062,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/098,565
FILING DATE: 1998-04-17
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                                                                                                             PatentIn Ver. 2.0
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No. US20030096779A1
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TION NUMBER: US/09/292,225
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APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILLE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR PILING DATE: 1998-09-02
PRIOR PILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/095,295
PRIOR APPLICATION NUMBER: 60/095,295
PRIOR APPLICATION NUMBER: 60/098,565
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US-10-218-743-18
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SOFTWARE: Pater
SEQ ID NO 15
FUNCTH: 555
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Publication No. US20030096779A1
GENERAL INFORMATION:
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Best Local :
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Best Local
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/098,909
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PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 09/062,013
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19; Conserv
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Pred. No. 2.9e-08;
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Pred. No. 3e-08;
0; Mismatches
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PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17

1998-04-17

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; ORGANISM: Dermatophagoides farinae
US-10-218-743-18
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CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT TILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR PPLICATION NUMBER: 60/096,909
PRIOR FILING DATE: 1998-09-02
PRIOR PPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
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Best Local
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                          CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
                                                                                                                                                    TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                         APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Dermatophagoides farinae
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95.0%;
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Pred. No. 3e-08;
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US-09-864-408A-5584

Sequence 5584, Application US/09864408A Publication No. US20040009474A1

GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A

RESULT 9

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PRIOR FILLING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILLING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILLING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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                                                                                                             Query Match
Best Local :
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/062,013
                                                                                                                                                                                   TYPE: PRT ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                  LENGTH: 509
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464 LPHPTDVHKYLVCEYIATPNGG 485
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                                         2 IPHPTNIHKYLVCESV---NGG 20
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                                                                                                               Similarity
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63.6%;
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                                                                                                           Score 82.5; DB 14; Pred. No. 0.00032;
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Pred. No. 0
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APPLICANT: Kovalic David K
APPLICANT: Caho Yihua
APPLICANT: Caho Yihua
APPLICANT: Caho Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION UNMERR: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 260412
LENGTH: 291
TYPE: no-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT;
; TYPE: PRT
; PRANISM: Glycine max
; PEATURE:
; CTHER INFORMATION: Clone ID: PAT_MRT3847_88411C.1.pep
US-10-424-599-272856
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US-10-424-599-272856
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Best Local Similarity
Matches 7; Conserv
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SEQ ID NO 272856
LENGTH: 60
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5584
LENGTH: 67
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Best Local Similarity
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CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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APPLICANT: Kovalic David
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PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                   ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: PAT_MRT3847_77175C.1.pep
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Pred. No.
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Pred. No.
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Query Match
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Query Match
Best Local Similarity
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                                                                               ; OTHER INFORMATION: Clone US-10-424-599-274767
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 274767
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LENGTH: 29
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APPLICANT: Dennis Flint
APPLICANT: Steven Gutteridge
TITLE OF INVENTION: 3-Deoxy-D-Manno-Octulosonic Acid 8-Phosphate Synthases
FILE REFERENCE: BB1512 USNA
CURRENT APPLICATION NUMBER: US/10/222,723
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/312,679
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTMARE: Microsoft Word Version 7.0A
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other TITLE OF INVENTION: Plants and Uses Thereof for Plant In FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La ROBA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(410)
OTHER INFORMATION: unsure at all Xaa locations
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            40.4%; ilarity 43.5%; Conservative
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47.18;
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              Score 46.5; D
Pred. No. 86;
4; Mismatches
                                                                                             PAT_MRT3847_90135C.1.pep
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Pred. No.
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Pred. No.
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GRANISM: Glycine max
FEATURE:
FOTHER INFORMATION: Clone ID: PAT_MRT3847_77177C.1.pep
US-10-424-599-260414
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US-10-424-599-260414
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322))B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 260414
LENGTH: 156
                                                                                                                                                                                       Query Match 40.0%; Score 46; DB 12; Length 156; Best Local Similarity 47.1%; Pred. No. 37; Matches 8; Conservative 5; Mismatches 4; Indels
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 232599
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)8
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ORGANISM: Glycine max
FEATURE:
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                                                                                              88 DIPIVIDVHETIHCEAV 104
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Listing first 45 summaries
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/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/backfilesi.pep:*
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                           US-09-292-225-35

US-09-292-225-38

US-09-257-8258-21

US-09-257-8258-20

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US-09-257-8258-20

US-09-402-515A-16

US-09-402-515A-16

US-09-30-181-4

US-09-38-352-5038

US-09-585-173B-4

US-09-585-173B-4

US-09-585-173B-4

US-09-585-173B-1

US-09-30-181-17

US-09-30-181-2

US-09-30-181-17

US-09-30-181-17
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US-09-292-225-11

US-09-292-225-15

US-09-292-225-18

US-09-292-225-18

US-09-292-225-41
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Patent No.
Sequence
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Sequence 11, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 17, Appli
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## ALIGNMENTS

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TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION UNMER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER FILING DATE: 1999-04-25
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER: 09-062,013
EARLIER FILING DATE: 1998-04-17
NUMBER: FILING DATE: 1998-04-17
NUMBER: FILING DATE: 1998-04-17
NUMBER: PATENTION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER: PATENTION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER: PATENTION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
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US-09-292-225-11
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Sequence 11, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Heber, Eric R.
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
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Best Local S
Matches 20
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APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
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Patent No. 6455686
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Pred. No. 4.7e-
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, LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-03
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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LENGTH: 19
TYPE: PRT
ORGANISM: Dermatophagoides farinae
                    GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                           Sequence 15, Appli
Patent No. 6455686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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19; Conserv
INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
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Pred. No. 1.6e-09;
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NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
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                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
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EARLIER FILING DATE: 1998-09-02
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                                                                                                                                                                                LENGTH: 55
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TYPE: PRT
ORGANISM: Dermatophagoides farinae
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                            1 DIPHPTNIHKYLVCESVNGG 20
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DIPHPTNIHKYLVCEFVNGG 531
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Pred. No. 1.6e-09;
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US-09-292-225-41
; Sequence 41, Applicate
; Patent No. 6455686
; GENERAL INFORMATION:

Application US/09292225

APPLICANT: McCall, Catherine A.

RESULT 6

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APPLICANT: Hunter, Shirley Wu
APPLICANT: Waber, Eric R.
ITILE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 1999-04-15
CURRENT FILING DATE: 1999-09-02
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
MUMBER OF SEQ ID NOS: 49
RESULT 8
US-09-292-225-38
; Sequence 38, Application US/09292225
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-35
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-41
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CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-03
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-03
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-07
EARLIER FILING DATE: 1998-04-07
EARLIER FILING DATE: 1998-04-07
EARLIER FILING DATE: 1998-04-07
EARLIER APPLICATION NUMBER: 09/082,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 509
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Best Local Similarity
Matches 14; Conserv
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SEQ ID NO 41
LENGTH: 490
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 LPHPTDVHKYLVČEYIATPNGG 466
                                                                                                                                                      464 LPHPTDVHKYLVCEYIATPNGG 485
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ilarity 63.6%;
Conservative
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                                                                                                                                                                                                                                                            Score 82.5; DB 4;
Pred. No. 2.8e-05;
4; Mismatches 1
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Pred. No. 2.7e-05;
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                                                                                                                                                                                                                                                                                                                      Length 509;
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GENERAL INFORMATION:
APPLICANT: POOVaiah, Bachettira W.
APPLICANT: Potvaiah, Bachettira W.
APPLICANT: Patil, Shameekumar
APPLICANT: Takezawa, Daisuke
ITILE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
FILE REFERENCE: 4630-51993
CURRENT APPLICATION NUMBER: US/09/257,825B
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US/08/655,352
PRIOR APPLICATION NUMBER: US/08/655,352
PRIOR FILING DATE: 1996-05-23
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 517
LENGTH: 517
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US-09-292-225-38
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CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
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GENERAL INFORMATION:
APPLICANT: MCCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 509
TYPE: PRT
                                                                                 Query Match 47.8%;
Best Local Similarity 58.8%;
Matches 10; Conservative
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Best Local
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NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                               ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 LPHPTDVHKYLVCEYIATPNGG 485
97
                                  3 PHPTNIHKYLVCESVNG 19
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PHPNVIHLYDVCEDPSG 113
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Pred. No. 2.8e-05;
4; Mismatches 1
                                                                                      Mismatches
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RESULT 10 US-09-329-350-35 ; Sequence 35, Application US/09329350 ; Patent No. 6184019 ; GENERAL INFORMATION:

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US-09-329-350-35
Query Match
Best Local Similarity
Matches 8; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 452 amin-
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                        MOLECULE TYPE: 1
ORIGINAL SOURCE:
ORGANISM: Mel:
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APPLICATION NUMBER: 1
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FILING DATE: 30-APR-1997
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
FILING DATE: Herewith
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-OCT-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-DEC-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60
FILING DATE: 17-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-OCT-1996
ATTORNEY/AGENT INFORMATION:
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                                                                          NAME/KEY: Protein
LOCATION: 1.452
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 NAME: Shea Jr., Timothy REGISTRATION NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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Paloheimo, Marja
Suominen, Pirkko
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40.0%;
ilarity 44.4%;
Conservative
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Lantto, Raija
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Vehmaanper , J
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                                                                            /label= 50K-cellulase-B
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Score 46; DB 3;
Pred. No. 20;
3; Mismatches
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US-08-933-711B-18
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PATENT NO. 6514724
GENERAL INFORMATION:
APPLICANT: McMahon, Andrew P.
APPLICANT: Chuang, Pao-Tien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 520
                                                                                                                                                                                                                                                        SEQ ID NO 18
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                                                                                                                                                                                                                                                                                                        FILE REFERENCE: HUV-024.01
CURRENT APPLICATION NUMBER: US/08/933,711B
CURRENT FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/026,155
PRIOR FILING DATE: 1996-09-20
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chuang, Pao-Tien
TITLE OF INVENTION: HEDGEHOG INTERACTING PROTEINS AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/257,825B CURRENT FILING DATE: 1999-02-25 PRIOR APPLICATION NUMBER: US 08/655,352 PRIOR FILING DATE: 1996-05-23 PRIOR APPLICATION NUMBER: US 60/014,743 PRIOR FILING DATE: 1996-03-28
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                                                                                                                                                                                                                     LENGTH: 59
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Takezawa, Daisuke
TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                    FEATURE:
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                                                               Local Similarity hes 7; Conserv
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                                 2 IPHPTNIHKYLVCESVNG 19
VDHPDNINLTILCSDSNG 373
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                                                                   Conservative
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                                                                                  Score 45;
Pred. No.
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Pred. No.
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RESULT 13

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FILE REFERENCE: 2292/0G135
CURRENT APPLICATION NUMBER: US/09/402,515A
CURRENT FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 231
TYPE: PRT
TYPE: PRT
ORGANISM: Agkistrodon contortrix contortrix
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TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REFERENCE: 16U 101 V1
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 585
TYPE: PRT
ORGANISM: Homo sapiens
US-09-930-181-4
                                                                                                                                                                                                                                                                           RESULT 15
US-08-738-413B-11
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; Sequence 16, Application US/09402515A
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Patent No. 6455292
GENERAL INFORMATION:
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GENERAL INFORMATION:
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TITLE OF INVENTION: ANTICOAGULANT FUSION PROTEIN ANCHORED TO CELL MEMBRANE
FILE REFERENCE: 2292/0G135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: RIESBECK, Kristian APPLICANT: DORLING, Anthony
                                                      APPLICANT: HWANG, Jae-Hoon
APPLICANT: KIM, Doo-Sik
APPLICANT: YUN, Yung-Dae
APPLICANT: MOON, Hong-Mo
TITLE OF INVENTION: A NOVEL CDNA OF DIRECT-ACTING
TITLE OF INVENTION: FIBRINOLYTIC SERINE PROTEASE
NUMBER OF SEQUENCES: 12
                                     CORRESPONDENCE ADDRESS:
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805 Third Avenue
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4; Mismatches
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Search completed: March 22, 2004, 07:03:53 Job time: 2.61201 secs
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Best Local Similarity
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FILING DATE: October 23, 1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Ludwid, S. Petter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0.36/0C539
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acid
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TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bothrops atrox m
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IMMEDIATE SOURCE:
CLONE: BATROXOBIN
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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 GenCore version 5.1.6
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hypX protein - Rhi
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#### ALIGNMENTS

R;Salles, C.; Valenti, P.; Darlamitsou, A.; Henderson, N.; Campbell, L.; Glover, submitted to the EMBL Data Library, May 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: Z17665
A;Accession: T13387

hypothetical protein 115C2.8 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 19-Jan-2001 C;Accession: T13387

#### C;Date: Varnat-Evot. Transcript C;Date: Varnat-Evot. R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, I C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. C.A.; Li, G. C., C.; Cansen, H. C., C.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; pMID:11130712 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-573 <STO> hypothetical protein F9L1.22 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001 A;Introns: 340/1 A;Note: EG:115C2.8 C;Superfamily: Drosophila melanogaster hypothetical protein 115C2.8 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-408 <CAT> 뮍 Ş A;Cross-references: EMBL:AL031581; NID:e1320978; PID:e1320993; PIDN:CAA20887.1 C;Genetics: A86287 A;Cross-references: GB:AE005172; NID:g5103826; PIDN:AAD39656.1; GSPDB:GN00141 A;Cross-references: FlyBase:FBgn0020381 Query Match Best Local Matches 47.6%; Local Similarity 40.0%; es 8; Conservation 1 DPAKGMSPPGFIVGEEGVLS 20 DPQEGFDPPTYLIGPDEELS 346 <u>ა</u> Score 50; I Pred. No. 4. Mismatches DB 2; 7; Length 408; Indels 0, Khaykin, E.; Kim, C Maiti, R.; Marziali Gaps O.; Alonso; Dewar, K. 0

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A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35400.1; PID:e27240; PID:g1813967 A;Note: this sequence was submitted to the EMBL Data Library, December 1989 A;Note: this reading frame extends between two stop codons and does not begin with a st C;Superfamily: human cytomegaloving humaning the colonians and does not begin with a st
                                                                                                                                                                                                                                                                                                                                                                                                         M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein UL41 - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87552
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C; Superfamily:
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; M.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        809804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005673; NID:g13423989; PIDN:AAK24415.1; GSPDB:GN00148
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8; Conserv
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                                                                                                                  AKGMSPPGFIVGEEG 17
                                                                        AKDLPPPGYRVGRRG
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                                                                                                                                                                                                                                                           human cytomegalovirus hypothetical protein
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Pred. No. 22;
4; Mismatches
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Pred. No.
                                                                                                                                                                  Score 45; DB Pred. No. 8.7; 2; Mismatches
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3.7;
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                                                              R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                 hypothetical protein APE1998 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: H72502
                                          A; Accession: H72502
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Status: preliminary Molecule type: DNA

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A;Gene: SSO0872
C;Superfamily: hypothetical protein AF1590
                                                                                                                                                                                                                                                                                                                                                                                                    R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Parrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-408 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
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C;Superfamily: Aeropyrum pernix hypothetical protein APE1990
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A;Experimental source: strain K1
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A; Residues: 1-111 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A99139
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                                              4 KGMSPPGFIVGEEG 17
                                                                                        Similarity
8; Conserv
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8; Conserv
EGSTPPSGIVGEKG 63
                                                                                             Conservative
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                                                                                                                 Score 44;
Pred. No.
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Pred. No.
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                                                                                                              42;
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J.; K
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probable pta protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #semisona rominia.
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A;Cross-references: DDB:AP000063; NID:g5105654; PIDN:BAA81008.1; PID:g5105696
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1998
C;Superfamily: hypothetical protein AF1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                      J.; Danganan, L.; Poundstone, P.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; At P.; Quan, G.; Kronmiller, B.; Arellano, A.; Montgomery, M.; Ow, D.; Nolan, M. submitted to the EMBL Data Library, June 1938
A;Authors: Trong, S.; Kobayashi, A.; Olsen, A.S.; Carrano, A.V.
A;Description: Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a serine A;Reference number: Z14696
                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T02672
R;Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz,
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R;Cole, S.T.; Brosch, R.;
; Connor, R.; Davies, R.;
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                                                                                    ;Map position: 19
;Introns: 93/2; 1:
                                                                                                                                                                                            ;Molecule type: DNA
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;Accession: T02672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Cross-references: GB:Z84724; GB:AL123456; NID:g3261708; PIDN:CAB06578.1; PID:g1817674
;Experimental source: strain H37Rv
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;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                  ;Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens
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Best Local
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Query Match
Best Local Similarity
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                                                              R31449
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                                                                                                                                                                          1-813 <LAM>
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                                                                                                                                                  EMBL: AC005175; NID: g3253116; PID: g3253120
                                                                                    174/1; 228/2; 266/3; 331/1;
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41.9%;
53.8%;
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Pred. No. 76;
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Pred. No. 42;
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Pred.
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                                                                                    372/1; 474/3;
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ARGVGPPGYTPGE 1229

RESULT

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A;Gene: Hox2b (Ç;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;802-858/Domain: homeobox homology <HOX1> F;1040-1096/Domain: homeobox homology <HOX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Klinge, B.; Ueberlacker, B.; Korfhage, C.; Werr, W. Plant Mol. Biol. 30, 439-453, 1996
A;Title: ZmHox: a novel class of maize homeobox genes A;Reference number: S65774; MUID:96189260; PMID:86052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-835 < RES>
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A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Yi, J.R.; Lu, S.; Fernandez-Checa, J.; Kaplowitz, N.
J. Clin. Invest. 93, 1841-1845, 1994
A;Title: Expression cloning of a rat hepatic reduced glutathione transporter with A;Reference number: I55603; MUID:94216535; PMID:8163683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway ra C;Date: 26-Jul-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-379,'S',381-1539 <WER>
A;Cross-references: EMBL:X89761; NID:g1143706; PIDN:CAA61910.1; PID:g1143707
                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A;Reference number: S72455
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S
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A;Accession: S72455
                                                                                                                                                                                                                                                                                                                                          R;Werr, W
                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid
A;Molecule type: mRNA
A;Residues: 1-1539 <KLI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reduced hepatic glutathione transporter with canalicular
                                                                                                                                                                                                                                                                 A;Status:
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Best Local S
Matches 9
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;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change;Accession: S65775; S72455
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AKGMSPPGFIVGE 15
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3; Mismatches
                                                    Score 44; DB 2;
Pred. No. 1.9e+0;
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RESULT 13
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A;Residues: 1-3224 <YOK>
A;Residues: 1-3224 <YOK>
A;Cross-references: EMBL:D42063; NID:g924266; PIDN:BAA07662.1;
A;Experimental source: cell type B-lymphocyte
R;Wu, J.; Matunis, M.J.; Krasmer, D.; Blobel, G.; Coutavas, E.
J. Biol. Chem. 270, 14209-14213, 1995
A;Title: Nup358, a cytoplasmically exposed nucleoporin with pep A;Reference number: A57545; MUID:95294031; PMID:7775481
A;Accession: A57545
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                   probable integral membrane protein Cj0263 [imported] - Campylobacter jejuni (C;Species: Campylobacter jejuni (C;Species: Campylobacter jejuni (C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C;Accession: F81444 C;Accession: F81444 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
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R;Yokoyama, N.; Hayashi, N.; Seki, T.; Pante, N.; Ohba, Nature 376, 184-188, 1995
A;Title: A giant nucleopore protein that binds Ran/TC4.
A;Reference number: $58884; MUID:95327194; PMID:7603572
A;Accession: $58884
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
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A;Residues: 1-776,'R',778-783,'R',785-3224 <WUA>
A;Cross-references: GB:L41840; NID:g857367; PIDN:AAC41758.1; PID:g857368
                                                                                           020222
                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-291 < PAR>
                                                                                                                                                                                                                                              A;Accession: F81444
A;Status: prelimina
                                                                                                                                                                                                                                                                                         A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy A;Reference number: A81250; MUID:20150912; PMID:10688204
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  Query Match
Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Gene: GDB:RANBP2; NUP358
;Cross-references: GDB:4642758; OMIM:601181
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                                                                                                                                                       ;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72731.1; PID:g69677;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                              Status: preliminary
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60-93/Domain: tetratricopeptide repeat homology <TT2>
450-471/Domain: leucine zipper #Etatus predicted <LEU-
3063-3224/Domain: cyclophilin homology <CYP>
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                                                                                                             Gene:
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h 41.0%;
Similarity 53.3%;
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47.4%;
  Score 43; DB;
Pred. No. 41;
2; Mismatches
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Pred. No.
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                                             Length 291;
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Gaps
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                                                                  Search completed: March Job time : 3.30072 secs
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A; Molecule type: DNA
A; Residues: 1-359 < COL>
A; Cross-references: GB: ALO10186; GB: AL123456; NID: g3261493;
A; Experimental source: strain H37Rv
C; Genetics:
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A;Gene: all4751
C;Superfamily: ATP-NAD kinase
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H70876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Notecus type: DNA
A; Molecule type: DNA
A; Residues: 1-305 < KUR>
A; Cross-references: GB: BA000019; PIDN: BAB76450.1;
A; Cross-references: STrain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2399
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change C;Accession: AG239 #sequence_revision 14-Dec-2001 #text_change C;Accession: AG239 R;Kaneko; T; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S. R;Kaneko; T; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.
                                                                                                                                                                                                                                                                                                                             A;Authors: Sgares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: H70876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein all4751 [imported] - Nostoc sp. C;Species: Nostoc sp. PCC 7120
                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                         Rajandream, M.A.; Ro
Nature 393, 537-544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: H70876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision
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M.; Yamada, M.; Yasuda, 1
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1357.597 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PTA MYCTU
RBP7_HUMAN
ZUPT CAMJE
PPN HAEIN
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# ALIGNMENTS

ene."; at. Gene 5] EQUENCE EQUENCE EQUENCE	SEQUENCE TISSUE=Ov MEDLINE=9 Wu G.S., Krantz I. Spinner N	RP SEQUENCE FROM N.A  RP LEU-32 AND VAL-67  RC TISSUS-Liver, and  RX MEDLINE-98039016;  RA Schneider P., Bod  RA Tschopp J.;  RT "Characterization  RL FEBS Lett. 416:32  RN [4]			0.0
18 d DWA Gamage-Inducibi 17:141-143(1997). M N.A. (ISOFORM SHORT). 0508; PubMed=9242610;	PubMed=9326928; F. McDonald E.R. G., Gan D.D., Zho Kowitz S., Wu G.,	. (ISOFORM LONG), Spleen; PubMed=9373179; mer JL., Thome M of two receptors 9-334(1997).	FROM N.A. (ISOFORMS LONG A AND VARIANTS LEU-32 AND V 431692; PubMed-9285725; 3.R., Mongkolsapaya J., Xu 3.R., Mongkolsapaya J., Xu 4.J., Bell J.I.; 1 new alternatively splice signal from TRAIL."; 1. 7:693-696(1997).	N.A. (ISOFORM LONG), in fibroblast; 2025; PubMed=9311998; 2025 Esposti M.A., Johnour M.S., Gerhart M.J. Rauch C.T.; Rauch C.T.; 2027/1027/2027/2027/2027/2027/2027/2027/	PRT; il7; O15; d) equence motatik oor supe: ptosis: ptosis: OR TRICE OR TRICE Crania ; Crania
סי וֹ	Jiang W., Meng R., Y., Muschel R., Hami Debry W.S.;	CHARACTERIZATION, AND VARIANTS  ., Hofmann K., Holler N., for TRAIL.";	ID SHORT), ALTERNATIVE LL-67. XN., Cowper A.E.,	AND SEQUENCE OF N-TERMINUS.  nson R.S., Smolak P.J., Waugh , Schooley K.A., Smith C.A., ing receptor for TRAIL.";	440 AA. 440 AA. supdate) update) on update) infamily member 10B precursor inducing ligand receptor 2) ( K2 OR KILLER OR ZTNFR9. Lata; Vertebrata; Euteleostomi rhini; Hominidae; Homo.

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahesley R.W., Toudman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schwinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Schwinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Schwinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Schwinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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J. Biol. Chem. 277
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"Homo sapiens homolog
Submitted (OCT-1999) t
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MEDLINE=98090092; PubMed=9430227;
Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Mu
"Death receptor 5, a new member of the TNFR family,
"Death receptor 5, a new member of the NFR family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Woo Goddard A.D., Godowski P., Ashkenazi A.; "Control of TRAIL-induced apoptosis by a family of sixeceptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FADD-dependent apoptosis and activate Immunity 7:821-830(1997).
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Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., Kelley R.F., Ashkenazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of Apocomplex with death receptor 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97390509;
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                                                                                                 MEDLINE=20017054; PubMed=10549288
                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
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ISOId=014763-2; Sequence=VSP_006490;

ITSSUE SPECIFICITY: Widely expressed in adult and fetal tissue very highly expressed in tumor cell lines such as Hela S3, K56 HL-60, SW480, A549 and G361; highly expressed in hearr, periph blood lymphocytes, liver, pancreas, spleen, thymus, prostate, ovary, uterus, placenta, testis, esophagus, stomach and through the intestinal tract, not detectable in brain.

-! INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
-! DISEASE: Defects in TWFRSF10B may be a cause of squamous cell carcinoma of the head and neck (HNSCC) [MIM:601400].
-! SIMILARITY: Contains 3 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specificity in apoptotic initiati
Nat. Struct. Biol. 6:1048-1053(1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Receptor for the cytotoxic ligand INFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine protesses) mediating apoptosis. Promotes the activation of NF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Long; Synonyms=TRICK2B;
IsoId=014763-1; Sequence=Displayed.
Name=Short; Synonyms=TRICK2A;
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AF016266;
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AF016268;
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AAF75587.
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   C:integral to membrane; IC. F:apoptosis activator activity; F:caspase activator activity; N
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_HCMVA
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H3
Chain H3) (Inter-alpha-inhibitor heavy chain
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Q63416;
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P16814;
SEQUENCE FROM N.A. STRAIN=Sprague-Dawley; Blom A., Fries E.;
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15-JUL-1998 (Rel.
28-FEB-2003 (Rel.
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SEQUENCE 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not
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Betaherpesvirinae; Cytomegalovirus.
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                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                               Rattus norvegicus
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141 AA; 16766 MW;
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nilarity 53.3%;
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Rodentia;
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Pred. No. 7.8;
                                                                                                    Craniata; Veri
Sciurognathi;
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Viruses; dsDNA viruses,
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                                                         SEQUENCE FROM N.A.
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(MAR-1989)

to the

EMBL/GenBank/DDBJ databases

(Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 16, Last annotation updat
26.8 kDa protein.

update)

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stage;

Lipothrixviridae;

(strain KRA1) (TTV1)

STANDARD;

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Query Match
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CARBOHYD
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                     InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                        Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                           EMBL; X83231; CAA58233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                PROSITE; PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: I-alpha-I plasma protease inhibitors are assembled fro one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H and bikunin, inter-alpha-like inhibitor (I-alpha-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin. PTM: Heavy chains are interlinked with bikunin via a chondroiti 4-sulfate bridge to the their C-terminal aspartate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the ITIH family. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
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SM00327; VWA; 1.
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                            DPAKGMSPPGFIVGEEG
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                                                       Conservative
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34
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N-LINKED (GLCNAC. . .)
CHONDROITIN 4-SULFATE,
(BY SIMILARITY).
(BY SIMILARITY)
                                                       4.
                                                                                                                                                                                   POTENTIAL.
BY SIMILARITY.
INTER-ALPHA-TRYPSIN 1
H3.
BY SIMILARITY.
                                                                   Score 45;
Pred. No.
                                                                                                                                                                           VWFA.
                                                   Mismatches
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A Strausberg R.D., Colling F.S., Wagner L., Schemmen C.M., Schuler G.D., A klausner R.D., Colling F.S., Wagner L., Schemmen C.M., Schuler G.D., A altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., A Hopkins R.F., Jordan H., Moore T., Kubin G.M., Hong L., Staplecon M.J., Usdin T.B., Fonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Mitting M., Madan A., Constant J., Wyers R.M., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Helton S.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local S
Matches
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rowen L., Qin S., Madan A., Loretz C., Hall J., James R., Dor:
Shaffer T., Abbasi N., Ratcliffe A., Dickhoff R., Lasky S., H
"Sequence of the mouse major histocompatibility complex class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X14855; CAA32992.1; -.
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MEDLINE=22388257; PubMed=124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003
15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129/SvJ;
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(Rel. 41, Last sequence update)
(Rel. 43, Last annotation updat
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Rodentia;
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                                                                                                           SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

MEDLINE-22206494; PubMed=12218036;

MEDLINE-22206494; PubMed=12218036;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;

"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phosphate acetyltransferase (EC 2.3.1.8) (Pho
PTA OR RV0408 OR MT0421 OR MTCY22G10.04.
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PROSITE; PS50082; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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                                           laboratory strains.";
J. Bacteriol. 184:5479-5490(2002)
-!- CATALYTIC ACTIVITY: Acetyl-Co
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01-OCT-1996 (Rel. 34, Last;
01-OCT-1996 (Rel. 34, Last;
28-FEB-2003 (Rel. 41, Last;
Ran-binding protein 2 (RanB)
(Nucleoporin Nup358) (358 kl
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InterPro; IPR004614; Pta.
InterPro; IPR002505; PTA, PTB.
InterPro; IP
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                                                                                                                                                                   Yokoyama N., Hayashi N., Seki T., Nishii K., Hayashida T.,
Kuma K.I., Miyata T., Fukui M., Nishimoto T., Pante N., Ae
"A giant nucleopore protein that binds Ran/TC4.";
Nature 376:184-188(1995).
                                                                                                                                                                                                                                                        TISSUE=Blood;
MEDLINE=95327194; PubMed=7603572;
                                                                                                                                                                                                                                                                                                                                                               MEDIINE=95294031; PubMed=7775481; Wu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E.; Wu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E.; "Nup358, a cytoplasmically exposed nucleoporin with peptide repeats, Ran-GTP binding sites, zinc fingers, a cyclophilin A homologous domain, and a leucine-rich region."; J., Biol. Chem. 270:14209-14213(1995).
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analogue: implications
Nature 398:39-46(1999)
                    Vetter I.R., Nowak C., Nishimoto T., Kuhlmann J., Witt "Structure of a Ran-binding domain complexed with Ran analogue: implications for nuclear transport.";
                                                                   Vetter I.R.,
                                                                                            X-RAY CRYSTALLOGRAPHY (2.96 ANGSTROMS)
MEDLINE=99176415; PubMed=10078529;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates;
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een the Swiss Institute of Bioinformatics and the EMBL outst
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-i- FUNCTION: Involved in transport factor (Ran-GTP, karyopherin) - mediated protein import via the F-G repeat-containing domain whice acts as a docking site for substrates. Could also have isomerase or chaperone activity and may bind RNA or DNA. Component of the nuclear export pathway. Specific docking site for the nuclear export factor exportin-1.
-I- SUBUNIT; Forms a tight complex in association with RANBP1 and the ubiquitin-conjugating enzyme E2 (UBC9) (By similarity).
-I- SUBCELLULAR LOCATION: Nuclear pore complex. Cytoplasmic filaments:
-I- DOMAIN: Contains F-X-F-G repeats.
-I- SIMILARITY: Contains 8 RANBP2-type zinc fingers.
-I- SIMILARITY: Contains 8 RANBP2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which
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filaments

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MIM; 601181; -.

GO; GO:0005643; C:nuclear pore; TAS.
GO; GO:0008536; F:RAN prothern binding; TA
GO; GO:0006606; P:protein-nucleus import;
InterPro; IPR002130; CSA PPIASe.
InterPro; IPR000697; EVHI.
InterPro; IPR000697; EVHI.
InterPro; IPR000156; Ran BPI.
InterPro; IPR000156; TPR-like.
InterPro; IPR000140; TPR.
InterPro; IPR001440; TPR.
InterPro; IPR001476; Znf RanGDP.
Pfam; PF00160; Pro_isomerase; 1.
Pfam; PF00160; Pro_isomerase; 1.
Pfam; PF00515; TPR; 1.
Pfam; PF00515; TPR; 1.
                                                                                                                                                                                                                                                                                                         PRINTS; PRO0153; CSAPPISMRASE.
SMART; SM00160; RanBD; 4.
SMART; SM00547; ZnF RBZ; 8.
SMOS4TE; PS00170; CSA PPIASE 1; 1.
PROSITE; PS50072; CSA PPIASE 2; 1.
PROSITE; PS50072; CSA PPIASE 2; 1.
PROSITE; PS50096; RANBD; 4.
PROSITE; PS001398; ZF RANBP2 1; 8.
PROSITE; PS00139; ZF RANBP2 2; 8.
Nuclear protein; Transport; Repeat; Z.
Nuclear protein; Transport; Repeat; Z.
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EMBL; D42063; BAA07662.1; -.
PIR; S58884; S58884.
PDB; 1RRP; 18-MAY-99.
Genew; HGNC:9848; RANBP2.
                                                                                                                                                                                                                                                                                               Nuclear protein;
3D-structure; Po
                                                                                                          VARIANT
                                                                                                                      1724
1781
2012
2309
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7AR_014886.
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                                                                                                                      CYCLOPHILIN-TYPE.
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RESULT 8
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Matches 9
                                                                                                 PIR, F81444;

PIR, F81444;

HAMAD; MF 00548; -; 1.

Therpro; IPR003689; Zn.

Therpro; Zip; 1.
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Q9PIN2;
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                    MEDLINE=20150912; PubMed=10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter je
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
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STRAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                    EMBL; AL139074; CAB72731.1; PIR; F81444; F81444.
                                                                                                                                                                                                                                                                                                                   Nature 403:665-668(2000)
                                                                                                                                                                                                                                                                                                                            reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc transporter zupT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
10-OCT-2003
                                                                   TRANSMEM
                                                                              Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   FUNCTION: Mediates zinc uptake. May also transpocations (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein SIMILARITY: Belongs to the ZIP transporter (TC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2505
                                                                                                                                                                                                                                                            subfamily.
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(Rel. 41, Last seq
(Rel. 42, Last ann
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174
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transport;

B 28
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7 124
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                                                                                        Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                               noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                       also transport
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                                                                                        Complete proteome
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                                                                                                                                                                                                                                                                      (TC 2.A.5) family. ZupT
                                                                                                                                                                                                                                                                                                                                         Campylobacter jejuni
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RESULT 10
BET3\_MESAU
ID BET3\_M
AC 009029
DT 30-MAY

BET3 MESAU 009029; 30-MAY-2000

(Rel. 39, STANDARD;

Created)

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Matches 8
                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cyanobacterium Anabaena sp. strain
DNA Res. 8:205-213(2001).
-!- FUNCTION: Catalyzes the phospho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe A., Iriguchi M., Ishikawa A., Kawash
Kishida Y., Kohara M., Matsumoto M., Matsuno J
Nakazaki N., Shimpo S., Sugimoto M., Takazawa
Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                        Pfam; PF01513; NAD_kinase; 1.
Transferase; Kinase; NAD; NADP;
SEQUENCE 305 AA; 32798 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: Divalent metal ions (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the NAD kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Cyanobacteria; Nostocales;
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable inorganic polyphosphate/ATP-NAD kinase 1 (EC 2.7.1.23)
(Poly(P)/ATP NAD kinase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPN1_AN
Q8YN19;
                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                PIR; AG2399; AG2399.
                                                                                                                                                                                                                                                                                                                                           EMBL; AP003597; BAB76450.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPNK1 OR ALL4751.
                                                                                                                                                                                                                                                              InterPro:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyphosphate as a source of phosphorus (By similarity). CATALYTIC ACTIVITY: AIP + NAD(+) = ADP + NADP(+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Catalyzes the phosphorylation of NAD to NADP. Utilizes ATP and other nucleoside triphosphates as well as inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANASP
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56
                                                                                                                                                                                                                                                           MF_00361; -; 1.
ro; IPR002504; ATP_NADK.
                                            N
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``
                                                                                            Similarity 30.88; Conservative
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                                            PAKGMSPPGF----IVGEEGVL
PIDGLTPPGFDSEMKFAIVLGGDGTV
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                                                                                         Score 43; DB
Pred. No. 31;
6; Mismatches
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Pred. No.
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31;
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ima K., Kimura T.,
A., Muraki A.,
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                                                                                                                                         Length 305,
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RESULT
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TAFFEEER SCCOX
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Best Local
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01-NOV-1995 (Re)
28-FEB-2003 (Re)
Protein HI1410
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                                                                                                                                                                                                                                                                                                                                                                                        DNA_BIND
Haemophilus influenzae,
Bacteria; Proteobacteria; Gan
Pasteurellaceae; Haemophilus,
NCBI_TaxID=727;
                                                                                                                                                                        HABIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S80870; AAB50691.1; -. TRANSFAC; T01674; -. InterPro; IPR001092; HLH_bas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurod1 and Myod-responsive genes, probably by heterodimerization with class a basic helix-loop-helix factors. Despite the presence of an intact basic domain, does not bind to DNA.

-!- SUBUNIT: HETERODIMER WITH OTHER BHLH PROTEINS, LIKE TCF3 (E47).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: Kidney, lung, brain and pancreas (insulinoma).
-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peyton M., Stellrecht C.M.M., Naya
Tsai M.-J.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                         P44184;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                               HI1410
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15-MAR-2004 (Rel.
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HELIX-LOOP-HELIX MOTIF.
POLY-ALA.
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Best Local S
Matches 9
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15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
Amino acid permease 2
AAP-2 OR AAP2.
                                    SEQUENCE FROM N.A.

Margolles-Clark E., Bowman B.J.;

Margolles-Clark E., Bowman B.J.;

Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

SUBCELLULAR LOCATION: Integral membrane protein (Probat-
-!- SIMILARITY: Belongs to the amino acid permease family.
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059942;
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Venter J.
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                                                                                                                                      Neurospora crassa.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;
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SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907.
This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
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InterPro; IPR006437; Phage_term_2.
Pfam; PF04466; G2P; 1.
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RESULT 13
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Best Local
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 90.8 kDa protein in RRP41-SNGI in
YGR196C OR G7589.
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                                                                                                                                                                                                                                          "The complete sequence of a 9000 bp fragment of the right arm Saccharomyces cerevisiae chromosome VII contains four previous unknown open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF053231; AAC08355.1;
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                                                                                                                                                                                                                                                                                                                       MEDLINE=96076633; PubMed=7502584;
Guerreiro P., Maia e Silva A., Barreiros T., Arroyo J.,
Garcia-Gonzalez M., Garcia-Saez M.I., Rodrigues-Pousada
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                                                          or send an email to license@isb-sib.ch)
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  CAA58019.1;
CAA97222.1;
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(See http://www.isb-sib.ch/announce/
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01-FEB-1994 (Rel. 28, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein R05D3.9 in Chromosome III
R05D3.9/R05D3.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Couls Enfited M., Burton J., Connell M., Copsey T., Cooper J., Couls Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier P. Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Jaurer B., O'Callaghar Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghar Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownk Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GermOnline; 141508; -.
SGD; S0003428; FYV8.
GO; GO:0005737; C:cytoplasm; IDA.
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                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. By and for commercial modified and this statement is not removed. Lugge by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
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NCBI_TaxID=6239;
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                                                                                                                                                          Hypothetical protein; Signal SIGNAL 1 29
                                                                                                                                                                                                            PIR; S44863; S44863.
PIR; S44865; S44865.
WormPep; R05D3.9; CE31049.
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                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
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646 AA;
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Score 42.5; D
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HYPOTHETICAL PROTEIN R05D3.9; 887932547DB5B141 CRC64;
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                                                 Length 646;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unu M.-L., Zhang R.-Z., Pan T.-C., Stokes D., Conway D., Kuo H.-J., Glanville R., Mayer U., Mann K., Deutzmann R., Timpl R.; "Mosaic structure of globular domains in the human type VI collagen alpha 3 chain: similarity to von Willebrand factor, fibronectin, actin, salivary proteins and aprotinin type protease inhibitors."; EMBC J. 9:385-393(1990).
                                                                                                                                                                                                                                                                                                                                                         Weil D., Mattei M.-G., Passage E., var
Mann K., Deutzmann R., Timpl R., Chu w
"Cloning and chromosomal localization
three chains of type VI collagen.";
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01-0CT-1989 (Rel. 12, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Collagen alpha 3(VI) chain precursor.
                                                                                                                                                                                                               alpha 3
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MEDLINE=89066644; Publ
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Mammalia; Eutheria; Primates;
                                      Olsen O., Petersen L., Ducruix A.; "The 1.6 A structure of Kunitz-type
                                                                               Arnoux B.,
                                                                                                       MEDLINE=95182468;
                                                                                                                             X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                            MEDLINE=93054780;
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246:609-617
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y D., Pan T.-C., B
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Scerensen M.D., Bjoern S., Norris James T.L., Led J.J.;
"Solution structure".
                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P12111-2; Sequence=VSP 001172;

-!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- DISEASE: Defects in COL6A3 are a cause of Bethlem myopathy (MIM:158810). BM is a rare autosomal dominant proximal myopathy characterized by early childhood onset (complete penetrance by age of 5) and joint contractures most frequently affecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=98204804; Pubmed=>,, Files Fan T.-C., Zhang R.-Z., Pericak-Vance M.A., Tandan R., Files Stajich J.M., Viles K., Vance J.M., Chu M.-L., Speer M.C.; Stajich J.M., Viles K., Vance J.M., Chu factor type A domain "Missense mutation in a von Willebrand factor type A domain "Missense mutation in a von Willebrand family with Bethlem
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Demir E., Sabatelli P., Allamand V., F.
Makrelouf M., Topaloglu H., Echenne B.
Makrelouf S. Topaloglu H., Echenne Congenital muscular dystrophy.";
Am. J. Hum. Genet. 70:1446-1458(2002).
                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a detween the Swiss Institute of Bioinformatics and the EMBL
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DISEAS: befects in COL6A3 are a cause of Ullrich congenital muscular dystrophy (UCMD) [MIM:254090]; also known as Ullrich scleroatonic muscular dystrophy. UCMD is an autosomal recessive congenital myopathy characterized by muscle weakness and multipl joint contractures, generally noted at birth or early infancy. I clinical course is more severe than in Bethlem myopathy.

SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

SIMILARITY: Contains 1 fibronectin type III domain.

SIMILARITY: Contains 12 VWFA domains.
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SUBUNIT: Trimers composed of three
alpha 2(VI), and alpha 3(VI).
ALTERNATIVE PRODUCTS:
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                                                               CAA36267.1; -. CAA29557.1; -.
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COLLAGEN ALPHA 3(VI) CHAIN.

NONHELICAL REGION.

TRIPLS-HELICAL REGION.

VWFA 1.

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CELL ATTACHMENT SITE.
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EG:115C2.8 OR CG13367.
EG:115C2.8 OR CG13367.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
  FlyBase;
SEQUENCE
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                          Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases EMBL; AE003418; AAF45535.1; -. EMBL; AL031581; CA20887.1; -. PIR; T13387; T13387.
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Salles C., Valenti
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01-MAY-2000 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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STRAIN=APCC 19718 / IFO 14298;

MEDLINE=2586410; PubMed=12700255;

MEDLINE=2586410; PubMed=12700255;

Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,

Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,

Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

"Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph Nitrosomonas europaea.";

J. Bacteriol. 185:2759-2773 (2003).
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01-OCT-2003
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Q82SJ2;
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Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., C
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538104; CAD98017.1; -.
Hypothetical protein.
SEQUENCE 118 AA; 12808 MW; 0310EF37E1F0E92C CRC64;
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Hypothetical protein DKFZp686I01145.
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Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu
Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
Altafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L.,
Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Pal
Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,
Federspiel N.A., Theologis A.,
"Arabidopsis thaliana chromosome 1 BAC F9L1 sequence.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO07591; AAD39656.1; -.
Theologis A.;
"Arabidopsis Full Length cDNA Clones.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ EMBL; AY080765; AAL87253.1; -
Hypothetical protein.
SEQUENCE 584 AA; 63284 MW; 5DD94B2B05B83B4
                                                                                                                                                                                                              Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Xim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledona; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
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Palm
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Ecker J.R.
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Matches
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SEQUENCE FROM N.A., Chang C.H., Dal Yamada K., Chan M.M., Chang C.H., Wa Quach H.L., Tang C.C., Toriumi M., Wa Yu G., Yuan S., Chen H., Cheuk R., Jo Palm C.J., Shinn P., Southwick A., Tr Ecker J.R., Theologis A.;

"Arabidopsis Open Reading Frame (ORF)
"Arabidopsis Open Reading Frame (ORF)
Submitted (SEP-2002) to the EMBL/GenB EMBL; AVI50428; AAVI2970.1; --
                                                                                                                                                                                                                                        Q8E7U2;
Q8E7U2;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8H1F3;
Q8H1F3;
invasive neonatal disease.";

Mol. Microbiol. 45:1499-15:13 (2002).

EMBL, ALTG6643; C.AD45698 1.; -.

SagaList; gbs0053; -.

GO; GO:001691; F:ixron ion binding; IEA.

GO; GO:001691; F:oxidoreductase activity;

GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                        Hypothetical GBS0053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis Italiana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots; rosid
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical AT1G15280.
                                                                                              Glaser P.,
Msadek T.,
                                                                                                       MEDLINE=22242508; PubMed=12354221; Glaser P., Rusnick C., Buchrieser
                                                                                                                               SEQUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
                                                                                                                                                                          Streptococcus.
                                                                                                                                                                                   Bacteria; Firmicutes;
                                                                                                                                                                                    Streptococcus agalactiae (serotype III) Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 585 AA; 6
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01-MAR-2003
                                                                                     Kunst F.;
                                                                                                                                                             NCBI_TaxID=216495;
                                                                          Genome sequence of Streptococcus
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Pred. No.
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Wallender E.K., Wong C., Wu H.,
Jones T., Kim C.J., Nguyen M.,
Tripp M.G., Wu T., Davis R.W.,
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                                                                                                         Chevalier
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73;
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InterPro; IPR001670; Fe-ADH.
Pfam; PF00171; aldedh; 1.
Pfam; PF00465; Fe-ADH; 1.
PROSITE; PS00913; ADH IRON 1; 1.
PROSITE; PS00060; ADH IRON 2; 1.
Complete proteome.
SEQUENCE 880 AA; 97005 MW; FC26D6B9
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InterPro; IPR001670; Fe-ADH.
Pfam; PP00171; aldedh; 1.
Pfam; PF00465; Fe-ADH; 1.
PROSITE; PS009913; ADH IRON 2; 1.
PROSITE; PS00060; ADH_IRON 2; 1.
Hypothetical protein; Complete pro
SEQUENCE 880 AA; 97005 MW; PC2
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STRAIN=2603 V/R / Serotype V;

MEDLINE=2222988; PubMed=12200547;

Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.

Messels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora I

Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione B., Mando D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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Aldehyde-alcohol dehydrogenase.
ADHE OR SAG0053.
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NCBI_TaxID=216466;
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GO; GO:000550; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity;
GO; GO:0008152; F:metabolism; IEA.
Q7X4K8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   emerging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative genomic analysis of smerging human pathogen, serotype V Streptococcus agalactiae.'eroc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M.;
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9; Conserv
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3; Mismatches 6
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Matches 7
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Gaitatzis N., Silakowski B., Kunze B
Hofle G., Muller R.;
"The biosynthesis of the aromatic myz
inhibitor stigmatellin is directed by
polyketide synthase.";
Submitted (MAR-2002) to the EMBL/Geni
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01-JUN-2002 (TremBLrel.
01-JUN-2003 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perelman A., Uzan A., Hacohen D., Schwarz R.;
"Oxidative Stress in Synechococcus sp. Strain PCC 7942: Various
Mechanisms for H(2)O(2) Detoxification with Different Physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPXA.
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0; GC:0006364; P:rNNA processing; I
InterPro; IPR000238; Rib_bind_factA.
fam; PF02033; RBFA; 1.
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Last sequence up
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Pred. No. 27;
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Pred. No.
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InterPro; IPR006680; Amidohydro 1.
InterPro; IPR004722; Pept M38_DHOmult.
InterPro; IPR005847; Pept M38_regn.
Pfam; PF01979; Amidohydro 1; 1.
Prodom; PD000518; Urease; 1.
TIGRDMs; TIGR00857; pyrC_multi; 1.
                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
Currie J., Collura K.;

"Rice Genomic Sequence.";

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC104473; AAN60993.1; -.

EMBL, AC104473; AAN60993.1; -.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl
GO; GO:0004553; F:hydrolase activity; IEA.

GO; GO:000575; F:carbohydrate metabolism; IEA.

InterPro; IPR00490; Glyco_hydro_17.

InterPro; IPR00490; Glyco_hydro_17.
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01-OCT-2003 (TEMBLrel. 25,
Putative glycosyl hydrolase,
OJ1626805,8.
                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI TaxID=39947;
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                                                                                 Pfam; PF00332; Glyco_hydro_17; 1.
Hydrolase.
SEQUENCE 455 AA; 47499 MW; 50
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MEDLINE=21173698;
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PROSITE; PS00455; AMP_BINDING; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 662 AA; 74544 MW; FC698FB9AEA2C107
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Oshima T., Kikuchi H.;
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#### SUMMARIES

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# ALIGNMENTS

RESULT 1
AAY52513
ID AAY5 Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; felcanine; veterinary; antibody; vaccine; immunisation. 16-APR-1999; WO9954349-A2 House dust mite allergen protein (map) A/B fragment map(3) AAY52513 standard; peptide; 20 AA. 28-OCT-1999. Dermatophagoides farinae. 22-FEB-2000 (first entry) AAY52513; 99WO-US008524. diagnosis; human; feline;

17-APR-1998; 13-MAY-1998; 02-SEP-1998; 98US-00062013. 98US-0085295P. 98US-0098909P.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber ER,

WPI; 2000-052700/04.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Claim 3; Page 69; 154pp; English.

Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWM -map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. The HMW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines,

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02-SEP-1998;
                                                                                                                                          Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWM -map) composition. The HWW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. The HWW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a protein of the prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1999;
                                    variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA
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Pred. No. 3.1e-09;
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Best Local S
Matches 20
                                                  allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                  Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mite allergenic protein isolated from Dermatophagoides, HMW-map protein, useful as a vaccine for treating mite
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                 06-AUG-2003
22-FEB-2000
                                                            AAY52535;
                                                                                         AAY52535 standard; protein; 490
                                                                                                                                                                                                                                                                                         Sequence 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 71; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Der HMW-map polypeptide #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU96326 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HESK-) HESKA CORP
                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA,
                                                                                                                                                                                                 ы
                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                   DPAKGMSPPGFIVGEEGVLS 20
                                                                                                                                                                   DPAKGMSPPGFIVGEEGVLS
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                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                farinae.
                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                            Score 105; DB 5;
Pred. No. 3.1e-09;
'; Mismatches 0;
                                                                                                                                                                   20
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RESULT 6
AAU96339
ID AAU9
XX
AC AAU9
XX

AAU96339 standard; protein; 490 AA

AAU96339;

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279

DPAKGMSPPGFITGEEGVLS

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                                                                                                                                       This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-490, the mature form of pDerp98-509, PDerp98-490 has a molecular weight of 98 kD, comprising 490 amino acids, and has a high degree of homology with the D. farinae mature 98 kD allergen, maps (ANY52525). Nucleic acid molecules encoding PDerp98-490 were isolated from a D. pteronyssius cDNA library by hybridisation with a probe cenoding the D. farinae high molecular weight map (HDM-map) composition. White allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively intest kits and as tools to recover desired dust mite allergens from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
                                    Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 147-149; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ38589, AAZ38590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dermatophagoides pteronyssinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
1 DPAKGMSPPGFIVGEEGVLS 20
                                      19;
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           igh molecular weight Dermatophagoides nucleic acid polypeptides modify an animals' hypersensitivy to mite allergens.
                                                                                                              490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hunter SW,
                                      Conservative
                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00062013.
98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Asn is N-glycosylated"
                                                     96.2%;
95.0%;
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                                      0
                                    Score 101; DB 3;
Pred. No. 4.1e-07;
0; Mismatches 1
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                                                                      Length 490;
                                      Indels
                                      0
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AAY52533
ID AAY5
XX AAY5
XX AAY5
XX O6-A
DT 06-A
DT 22-F
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KW hous
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Der HMM-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
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                             Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgB; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                   06-AUG-2003
22-FEB-2000
                                                                                                                                                                                                     AAY52533;
                                                                                                                                                                                                                                     AAY52533 standard; protein; 509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated mite allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 144-146; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mite allergenic protein isolated from Dermatophagoides, designa
Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000; 2000US-00662293
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                                                                                                                 pteronyssius 98 kD mite allergen protein (map) PDerp98-509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-351888/38
                                                                                                                                                                                                                                                                                                                         279
                                                                                                                                                                                                                                                                                                                                                                                           19;
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                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                 DPAKGMSPPGFIVGEEGVLS 20
                                                                                                                                                                                                                                                                                                                         DPAKGMSPPGFITGEEGVLS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide #26
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           96.2%;
                                                                                                                                                                                                                                                                                                                                                                                        Score 101; DB 5;
Pred. No. 4.1e-07;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 490;
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15-JUL-2002

(first entry)

AAU96337;

AAU96337 standard; protein; 509

0

Der HMW-map polypeptide #24

Der HMW-map; American house dust mite; antiallergic; mite; I mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.

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                           S
                                                                                                                                                  This sequence represents Dermatophagoides pteronyssius mite allergen CC protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD, CC comprising 509 amino acids, and has a high degree of homology with the D CC farinae 98 kD allergen, maps (AAYS2523). Nucleic acid molecules encoding PDerp98-509 were isolated from a D. pteronyssius cDNA library by CC hybridisation with a probe encoding the D. farinae high molecular weight CC map (HMW-map) compositions with a literaphic proteins and peptides, and CC mucleic acids encoding them, may be used in therapeutic compositions to CC modify an animal's hypersensitivity reaction to make allergens. Animals CC that may be treated include mammals and birds, especially felines, and CC canines, equines, humans, other pets, and work or domestic animals. The proteins and peptides can also be used to raise antibodies, CC which have a variety of potential uses. For example, they can be used as CC vaccines to passively immunise animals against dust mite CC recover desired dust mite allergens from a mixture of proteins. (Updated CC on 06-AUG-2003 to correct OS field.)
                                                              Matches
                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1999
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                                                                                                                           Sequence 509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 134-136; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ38585,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-052700/04.
298 DPAKGMSPPGFITGEEGVLS 317
                               1 DPAKGMSPPGFIVGEEGVLS
                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hunter SW,
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00062013.
98US-0085295F.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ38586,
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                                                                           96.2%;
95.0%;
                                                            Score 101; DB 3;
Pred. No. 4.2e-07;
0; Mismatches 1
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                               20
                                                                                            Length 509;
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RESULT 9
AAU96338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                            Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 509 AA;
                                                       14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                  Dermatophagoides
                                                                                                                                                                                                                                                                                                                                                                                                                   Der HMW-map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 134-136; 161pp; English.
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                                                                                                                      21-MAR-2002
                                                                                                                                                                                 WO200222807-A2.
14-SEP-2000;
                                                                                                                                                                                                                                                                                                immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cal Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPAKGMSPPGFITGEEGVLS 317
                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORP
                                                                                                                                                                                                                                            farinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 5;
Pred. No. 4.2e-07;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein in useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgB, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANU96314-AAU96342
                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 139-141; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mite allergenic protein
Der HMW-map protein, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABK69583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-351888/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mccall CA,
                                                                                     represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated mite allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA CORP
                                              509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hunter SW,
                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolated from Dermatophagoides, designa as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ER;
Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         designated
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á 밁 Query Match Best Local S Matches 19 298 19; Similarity DPAKGMSPPGFIVGEEGVLS DPAKGMSPPGFITGEEGVLS Conservative 96.2%; ç. Score 101; DB 5; 1 Pred. No. 4.2e-07; D; Mismatches 1; 317 20 Indels 0; Gaps 0

RESULT 10
AAY52525
ID AAY52525
XX AAY52
XX AAY52
XX House
XX Mite
XX House
XX House
XX Lypex
XX Lypex
XX Lypex
XX Lypex
XX House
XX House nouse dust mite; IgE; immunoglobulin E; allergen; maph; maph; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation. House dust mite (D. farinae) mite allergen protein (map) PDerf98-536 AAY52525 standard; protein; 536 WO9954349-A2. Dermatophagoides farinae. Mite allergen protein; map; high molecular weight; HMW-map; allergy; 22-FEB-2000 AAY52525; 28-OCT-1999. (first entry) ž

17-APR-1998; 13-MAY-1998; 02-SEP-1998;

98US-00062013. 98US-0085295P. 98US-0098909P.

16-APR-1999;

99WO-US008524

WPI; 2000-052700/04 N-PSDB; AAZ38579, A

AAZ38580

Mccall CA,

Hunter SW,

Weber ER;

(HESK-) HESKA

CORP

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RESULT 11
AAU96329
ID AAU96
XX AU96
XX AU96
XX AU96
XX Der H
XX Der H
XX Der H
XX Der H
XX Mite
FN WO200
XX Derma
XX Derma
XX Index H
MC200
XX H
PR 14-SE
XX H
PR 14-SE
XX NPSI
PR N-PSI
PR N-PSI
XX NPSI
PR N-PSI
XX NPSI
PR N-PSI
XX NPSI
PR N-PSI
XX NPSI
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents Dermatophagoides farinae mite allergen protein (map) pDerf98-536, the mature form of pDerf98-555 (AAX52522). pDerf98-536 has a molecular weight of 98 kD, comprising 536 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each creation being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. White allergency proteins and compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or composition to mother proteins via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as veccines to passively immunise animals as adaptose mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Der HMW-map; American house dust mite; antiallergic; mite; I mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Der HMW-map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 536 AA;
                                                                                        Claim 12; Page 125-127; 161pp; English
                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                          Mccall CA, Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200222807-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dermatophagoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA CORP.
                                                                                                                                                   mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                  2002-351888/38.
DB; ABK69575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPAKGMSPPGFIVGEEGVLS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPAKGMSPPGFISGEEGVLS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125-127; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 99; I
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                          띥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; 1
9.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IgE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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The invention relates to

an

isolated mite allergenic protein

This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD,

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RESULT 12
AAY52523
IID AAY52
AXY52523
AC AAY52
XX AAY52
XX House
XX House
XX House
XX hype
XX hype
XX hype
XX hype
XX Derr
XX Cani
XX Oerr
XX Y
YN WO
XX Oerr
XX Y
YN WO
XX Oerr
XX Y
YN WO
XX Y
PN WO
XX OF
PN WO
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a noncomprisition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A compression of the rapeutic composition is useful for desensitising a host animal to an callergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a compression of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-1998;
13-MAY-1998;
02-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      House dust mite (D. farinae) mite allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY52523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dermatophagoides farinae
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                                                                                   Claim 3; Page 111-113; 154pp; English
                                                                                                                                            Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                      N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578
                                                                                                                                                                                                                                                                                                                          Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9954349-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   canine; veterinary; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                    2000-052700/04.
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                                                                                                                                                                                                                                                                                                                          Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00062013.
98US-0085295P.
98US-0098909P.
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/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Signal peptide
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555
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                                                                                                                                                                                                                                                                                                                             Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
5
5
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Pred. No. 9.1e-07;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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RESULT 13
AAU96327.
ID 96327.
AC AAU96
XX AAU966
XX Der H
XX Der H
XX Der H
XX Der H
XX M mite
KW 14-SI
PR 14-SI
YX 14-SI
YX MPI;
DR N-PSI
XX WPI;
DR N-PSI
XX WPI;
DR N-PSI
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Best Local 9
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                                                                                                                                                                                                              New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mite allergenic protein; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
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                                                                                                                                                                                                                                                                        N-PSDB; ABK69571.
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                                                                                                                                                                                                                                                                                                                         Hunter SW,
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HWW-map antibodies in animal fluids, and inhibition

Query Match

94 . %

Score

99;

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Length

555;

Sequence

Page 114-116; 161pp; English

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                      The invention relates to an isolated mite allergenic protein of CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-CC proteinaceous epitope is useful for identifying an animal (e.g., dog, CC cat) susceptible to or having an allergic response to a mite. An CC therapeutic composition is useful for desensitising a host animal to an CC dilergic response to a mite. The DNA and protein can be used in the CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition CC disease. Antibodies that bind to Der HMW-map grotein activity associated with a CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting CC binding of proteins to IgE, to prevent immunocomplex formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines CC against mite allergen hypersensitivity. Sequences ANU96314-ANU96342
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                                                                                                                                                                                                                                                                                                                                            New mite allergenic protein isolated from Dermatophagoides, designa Der HMW-map protein, useful as a vaccine for treating mite allergy.
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N-PSDB; ABK69573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2000; 2000US-00662293
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                                                       Query Match 47.6%; Score 50; DB Best Local Similarity 40.0%; Pred. No. 33; Matches 8; Conservative 5; Mismatches
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                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABI30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                  Sequence 488 AA;
                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 31035; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and interactions.
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
N-PSDB; ABL12184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC, Adams M,
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11-JUL-2000; 2000US-00614150.
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407 DPQEGFDPPTYLIGPDEELS 426
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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                                           1049977 seqs, 258955339 residues
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 4, Appli
Sequence 13, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 38, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 183401,
Sequence 181344,
Sequence 6, Appli
Sequence 2, Appli
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09-738-626-640	-10-425-114-5729	-10-424-599-	99-16974	-10-333-712-	0-314-410-	-09-811-088	-757-421-	-423-4	-10-333-71	-10-292-486-	-10-139-785-	-10-322-67	-10-288-917-	-10-242-383-	-10-314-410-	-10-207-655-	-10-076-773-	0-076-	-10-052-798-	-10-067-615-	-10-005-842-	-10-039-785-	S-10-211-462	-09-992-964-1	-09-611-088-	-09-887-879-	4-138-	-09-757-421	9-
quence 640	equence 57	equence 26	e 16	equence 3,	equence 4, Appl	4	quence 2, Appli	o L	equence 4, Appl	equence 3, Appl	equence 3, Appl	e 3, Appl	equence 1, Appl	H	6, Appl	)4, Ap	2, Appl	Sequence 2, Appli	1, Appl	2, Appl	2, Appl	3, Appl	equence 67	e 11,	ტ ტ	e 11,	e 2,	е4,	Sequence 2, Appli

### ALIGNMENTS

Sequence 4, Application US/10218743 Publication No. US20030096779A1

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TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/9/292,225
PRIOR PILING DATE: 1990-04-15
PRIOR PILING DATE: 1990-04-15
PRIOR PILING DATE: 1998-09-02
PRIOR PILING DATE: 1998-09-02
PRIOR PILING DATE: 1998-09-02
PRIOR PILING DATE: 1998-09-03
PRIOR PILING DATE: 1998-09-05-13
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR PILING DATE: 1998-04-17
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                                                                                                                                                        Query Match
Best Local :
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                                                                                                                                                                                                                                                                   LENGTH: 20
TYPE: PRT
ORGANISM: Dermatophagoides farinae
                                                   1 DPAKGMSPPGFIVGEEGVLS 20
                                                                                                                                                        Similarity
DPAKGMSPPGFIVGEEGVLS
                                                                                                                    100.0%; ilarity 100.0%; Conservative (
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                                                                                                                    Score 105; DB 14;
Pred. No. 7.6e-09;
; Mismatches 0;
20
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                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/088,909
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
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PRIOR APPLICATION NUMBER: 60/096,565
PRIOR APPLICATION NUMBER: 60/096,565
JS-10-218-743-41
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
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  TYPE: PRT ORGANISM: Dermatophagoides farinae
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                                                                      ENGTH: 490
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LENGTH: 509
TYPE: PRT
ORGANISM: Dermatophagoides farinae
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Best Local
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                          APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USBS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
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                                                                             PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
                                                                                                                    PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
                                                                                                                                                                                                                                           FILE REFERENCE: AL-2-C3
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FILING DATE: 1998-04-17
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FILING DATE: 1998-05-13
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                                     APPLICATION NUMBER: 60/098,565 FILING DATE: 1998-04-17
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19; Conserv
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ICATION NUMBER: 09/062,013
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; Pred. No. 9.8e
0; Mismatches
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Pred. No. 9.4e-07;
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US-10-218-743-15; Sequence 15, Application US/10218743; Publication No. US20030096779A1
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US-10-218-743-38
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SEQ ID NO 38
LENGTH: 509
TYPE: PRT
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LENGTH: 536
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/098,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Dermatophagoides farinae
-10-218-743-21
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Publication No. US20030096779A1
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APPLICANT: Hunter, Shifley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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PRIOR FILING DATE: 1998-09-02
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Local Similarity 95.0%;
hes 19; Conservation
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95.0%;
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Pred. No. 2
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Pred. No. 9.8e-07
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US-10-424-599-238601
; Sequence 238601, Application US/10424599
; Publication No. US20040031072A1
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Applica Publication No. US20 GENERAL INFORMATION:
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LENGTH: 555
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                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                                         ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                               LENGTH: 555
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                                                                                                                 298 DPAKGMSPPGFISGEEGVLS 317
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                                                                                                                                                DPAKGMSPPGFIVGEEGVLS 20
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Pred. No. 2.
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Pred. No. 2
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GENERAL INFORMATION: APPLICANT: La Rosa Thomas

APPLICANT:

T: Kovalic David K
T: Zhou Yihua
T: Cao Yongwei
INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

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US-09-925-302-483
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 238601
LENGTH: 143
TYPP- NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 181344
LENGTH: 69
TYPE: PRT
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 483
LEUGTH: 57
TYPE: PRI
                                                                                                                                                                                                                                                         Sequence 483, Application US/09925302 Patent No. US20020044941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 181344, Application US/10424599
Publication No. US20040031072A1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                               CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2003-04-28
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TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: PAT_MRT3847_134769C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_57482C.1.pep
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8; Conser
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Pred. No. 11;
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Pred. No. 6.8;
2; Mismatches 1
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                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-754-6
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                                                          Query Match
Best Local S
Matches 7
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Publication No. US20020161195A1

GENERAL INFORMATION:

APPLICANT: Alhemri, Emad S.

TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                 SOFTWARE: PatentIn SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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LENGTH: 350
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Publication No. US20020115154A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: MOYEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 480140.432D1
CURRENT APPLICATION NUMBER: US/10/067,615
CURRENT FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 6
SOPTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                               FILE REFERENCE: 480140.432D3
CURRENT APPLICATION NUMBER: 1
CURRENT FILING DATE: 2002-03
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                      LENGIH: 350
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 76
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                              2 PAKGMSPPGFIVGEEG 17
                                                                            Similarity
PSEGLCPPGHHISEDG
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                                                             Conservative
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                                                                            45.7%;
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43.8%; Pred. No. 55;
tive 5; Mismatches
 91
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                                                            Score 48; DB Pred. No. 55; Mismatches
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Pred. No. 7.8;
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3-
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RESULT 14 US-10-076-773-6

Sequence 6, Application US/10076773 Publication No. US20020161196A1 GENERAL INFORMATION:

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Gaps

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FILE REFERENCE: 480140.432D2
CURRENT APPLICATION NUMBER: US/10/076,773
CURRENT FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-10-076-773-6
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US-08-916-625B-2
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Best Local Similarity 43...
7; Conservative
                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: lines
Query Match
Best Local Similarity
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                                                                                                                                                                                                                          APPLICATION UNBER: US/08/916,625B
FILING DATE: 22-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/853,684
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/041,230
FILING DATE: 14-MARCH-1997
APPLICATION NUMBER: 610-41,230
FILING DATE: 14-MARCH-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50008-1
TELECOMMUNICATION INFORMATION:
TELECAX: 610-407-0701
TELECAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATMER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 19482
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: FASTERM: DOS
SOFTWARE: FASTESE for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: DEEN, KEITH C. PPLICANT: YOUNG, PETER R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE OF INVENTION: TUMOR NECROSIS FACTOR RELATED LE OF INVENTION: RECEPTOR, TR6
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 45.7%;
43.8%;
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 Score 48;
Pred. No.
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 DB 8;
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                   Length 411;
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Matches 7; Conservative 5; Mismatches 4; Indels

Qy 2 PAKGMSPPGFIVGEEG 17

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Db 76 PSEGLCPPGHHISEDG 91
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Search completed: March 22, 2004, 07:45:48
Job time: 4.09116 secs

3. J

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 g
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        on:
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                                          41.5
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Match Length
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Gapop 10.0 , Gapext 0.5
       US-09-662-293-4
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FOTUS_COMB.pep:*
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34, Appli 35, Appli 35, Appli 31, Appli 31, Appli 31, Appli 31, Appli 32, Ap
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US-09-252-991A-21650	US-09-107-532A-6265	US-08-401-512-53	US-09-252-991A-26412	US-09-252-991A-32847	US-09-043-627-6	US-09-543-681A-5442	US-08-459-065-3	US-08-459-146-3	US-09-328-352-5542	US-09-252-991A-17298	US-09-198-452A-458	US-08-821-118-5	US-08-821-119-17	US-09-489-039A-11591	US-09-543-681A-5516	US-09-711-164-349	US-09-252-991A-21851
Sequence 21650, A	e 6269	Sequence 53, Appl	Sequence 26412, A	Sequence 32847, A	Sequence 6, Appli	Sequence 5442, Ap	Sequence 3, Appli	Sequence 3, Appli	e 55	Sequence 17298, A	e 458,	Sequence 5, Appli	e 17, <i>l</i>	e 115	ō	Sequence 349, App	Sequence 21851, A

# ALIGNMENTS

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RESULT 2
US-09-292-225-13
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US-09-292-225-4
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
               Sequence 13, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
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Best Local s
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EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 20
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Patent No. 6455686
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
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Pred. No. 1.6e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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                                                                                                                                                       US-09-292-225-35
                                                                                                                                                                         RESULT 4
Sequence 35, Application US/09292225
PATENT NO. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
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LENGTH: 20
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Best Local
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LENGTH: 490
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Best Local Similarity
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EARLIER APPLICATION NUMBER: 60/035,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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SOFTWARE: PatentIn Ver. 2
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EARLIER APPLICATION NUMBER: 60/098,909
TABLIER FILING DATE: 1998-09-02
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SOFTWARE: Patentin Ver. :
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Pred. No. 2
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Pred. No. 1.6e-10;
Mismatches 0;
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2.7e-08;
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US-09-292-225-21

Sequence 21, Application US/09292225 Patent No. 6455686 GENERAL INFORMATION:

APPLICANT: McCall, Catherine A.

RESULT 6

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EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 35
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EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
SEQ ID NO 38
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Patent No. 6
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Best Local
                                                                              Matches
                                                                                                                   Query Match
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
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EARLIER FILING DATE: 1998-04-17
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                                                                                                                                                                                 TYPE: PRT ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                  Local
298
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                                                                            l Similarity
19; Conserv
                                  1 DPAKGMSPPGFIVGEEGVLS
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DPAKGMSPPGFITGEEGVLS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09292225
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                                                                                 Conservative
                                                                                               96.2%;
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                                                                                                  Score 101; DB 4;
Pred. No. 2.8e-08;
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Pred. No. 2
                                                                                 Mismatches
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                                                                                                                   Length 509;
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                                                                                 Indels
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RESULT 8
US-09-292-225-18
, Sequence 18, Application US/09292225
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-15
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; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
RUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                          Query Match
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Patent No. 6455686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                               LENGTH: 555
                                                                                                                                                                                                                      Local
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                                                                                                                298
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                                                                                                                                          1 DPAKGMSPPGFIVGEEGVLS 20
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                                                                                                            DPAKGMSPPGFISGEEGVLS 317
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95.0%;
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Pred. No. 6.6e
0; Mismatches
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Pred. No. 6.3e-08;
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FITIE OF INVENITOR: AL-2-C3
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1990-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1990-02
EARLIER FILING DATE: 1990-05-13
EARLIER FILING DATE: 1990-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1990-04-17
EARLIER FILING DATE: 1990-04-17
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 555
TYPER: PRI
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US-09-329-633A-2
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US-09-134-618-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Alnemri, E
TITLE OF INVENTION: N
TITLE OF INVENTION: N
                                                     Sequence 2, Application US/09329633A PATENT NO. 6252050
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 480140.432
CURRENT APPLICATION NUMBER: US/09/134,618
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
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APPLICANT: Kim, K. Jin
TITLE OF INVENTION: MET
TITLE OF INVENTION: CRO
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 350
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                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
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                                                                                                                                                                                                                               PSEGLCPPGHHISEDG
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emad S.
NOVEL TRAIL RECEPTORS,
METHODS OF USE THEREOF
 METHOD FOR MAKING MONOCLONAL ANTIBODIES CROSS-REACTIVE ANTIBODIES OBTAINABLE BY
                                                                                                                                                                                                                                                                                                    45.7%; Score 48; DB
43.8%; Pred. No. 6.7
tive 5; Mismatches
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6.7;
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   METHOD
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; NAME/KEY: xaa
; LOCATION: 410
; OTHER INPORMATION: xaa = leu or met
US-09-329-633A-2
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                                                                                                                             US-09-079-029-1
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PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
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                                                                             Best
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                                                            Matches
                                                                                            Query Match
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CURRENT APPLICATION NUMBER: US/09/329,633A
CURRENT FILING DATE: 1999-06-10
DRTOR APPLICATION NUMBER: US 60/089,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 411
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/09/079,029
APPLICATION NUMBER: US/09/079,029
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                         NAME: Marschang, Diane L.
REGISTATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 91:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                          Local Similarity nes 7; Conserv
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STREET: 1
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                            TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                              2 PAKGMSPPGFIVGEEG 17
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PSEGLCPPGHHISEDG 91
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Ashkenazi, Avi J.
                                                              Conservative
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                                                                             45.7%;
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Pred. No. 8;
                                                                             Score 48;
Pred. No.
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                                                                                               DB 4;
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RESULT 12
US-09-134-618-2
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Query Match
Best Local Similarity
Matches 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-039-785-3
                                                                                            ; ORGANISM: Homo sapiens US-10-039-785-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: MOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 480140.432
CURRENT APPLICATION NUMBER: US/09/134,618
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09134618 Patent No. 6417328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Salcedo et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                        SOFTWARE:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 66 SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL TITLE OF INVENTION: Receptors FILE REFERENCE: PF550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/323,807
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                  TYPE: PRT
                                                                                                                                                        JENGTH: 411
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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Similarity 43.8%;
7; Conservative
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                45.7%;
nilarity 43.8%;
Conservative 5
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Pred. No.
                    Score 48; DB Pred. No. 8; 5; Mismatches
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                                                        DB 4;
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76 PSEGLCPPGHHISEDG 91

Sequence 2, Application US/09333593A

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FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 199-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/953,684
PRIOR FILING DATE: 1997-08-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR APPLICATION NUMBER: 50/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 424
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PRIOR FILING DATE: 1997-08-22
PRIOR PLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 3.0
                                     ; TYPE: PRT; CORGANISM: HOMO SAPIENS
US-09-333-593A-8
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TYPE: PRT
ORGANISM: HOMO SAPIENS
-09-333-593A-2
  Query Match
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Patent No. 6313269
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APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
CURRENT FILING DATE: 1999-06-15
CURRENT APPLICATION NUMBER: 08/916,625
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APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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ROSHAK, AMY K.
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ROSHAK, AMY K.
45.7%; Score 48; DB 4; Length 424;
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Best Local Similarity 43.8%; Pred. No. 8.3;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps

Cy 2 PAKGMSPPGFIVGEEG 17

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Db 76 PSEGLCPPGHHISEDG 91
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Search completed: March 22, 2004, 07:03:54 Job time : 2.61201 secs

Run

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OM protein -

Title: Perfect score:

Scoring table: Sequence:

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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1 DEKNSFECILGP 1
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd
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F88028
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A;Accession: T20324
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-181 <WIL>
                                                                                                                                                                                                                                                                                                                                hypothetical protein D1086.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20324
R;Smye, R.
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T20324
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A;Molecule type: DNA
A;Residues: 1-180 <STO>
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Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Tote: genome with sequence 200; MUID:99069613; PMID:9851916
A;Note: genome with sequence with sequence 200; MUID:99069613; PMID:9851916
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F88028
                                                                                                                                    A;Cross-references: EMBL:Z81491; PIDN:CAB04020.1; GSPDB:GN00023; CESP:D1086.2 A;Experimental source: clone D1086 C;Genetics:
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                                                                     A; Map position: 5
A; Introns: 42/3; 135/3
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A;Map position:
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1; Mismatches
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      42;
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39 403 187 213 234 234 2531 2703

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Minimum DB Maximum DB

seq length: seq length:

Post-processing:

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Total number of

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C;Species: Vibrio cholerae
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998
C;Accession: S70808
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A;Description: The complete sequence of Ureaplasma u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iron(III) dicitrate transport ATP-binding protein UU069 [imported] - Ureaplasma urealyticum C; Species: Ureaplasma urealyticum
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A; Title: Use of recombinase gene fusions to A; Reference number: 870798; MUID:96414469;
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A; Residues: 1-291 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ivi protein VI - Vibrio cholerae (fragment)
N;Alternate names: cysA protein homolog
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                 Nature 406,
                                                R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: F82938;
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                                                                                           ;Species: Vibrio cholerae;Date: 18-Aug-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:AE002106; GB:AF222894; NID:g6899011; PIDN:AAF30474.1; GSPDB:GN001
Experimental source: serovar 3; biovar 1
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                                                                                                                                                                                                                                                                                                                                                                                   ;Molecule type: DNA
;Residues: 1-39 <CAM>
                                                                                  Accession: H82440
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                                                                                                                                                                                                                                                                                                                              Query Match
                 R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, ture 406, 477-483, 2000
                                                                                                                                       transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                              Local Similarity
les 7; Conserv
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 DNA
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8; Conserv
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                                                                                                                                  ATP-binding protein VCA0602 [imported] - Vibrio cholerae (strain
                                                                                                                                                                                                                                                                                               Conservative
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of both chromosomes
                                                                                                                                                                                                                                                                                                              59.7%;
63.6%;
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                                                                                                                                                                                                                           16
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Pred. No. 7.6;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusions to identify Vibrio 96414469; PMID:8817490
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of the cholera pathogen Vibrio cholerae.
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                                                Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
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G69164
hypothetical protein MTH493 - Methanobacterium thermoautotrophicum (strain Delta C;Species: Methanobacterium thermoautotrophicum
C;Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
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A; Map position: 2
C; Superfamily: unassigned
A;Gene: pyrE; BU559
C;Superfamily: orot
C;Keywords: glycosy
                                                                                                                                                                                                                                                                               orotate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Buchnera sp. (C;Species: Buchnera sp. (C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: A84995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-187 <MTH>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: G69164
R; Smith, D.R.; Douce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE004390;
A;Experimental source: serogroup
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A; Residues: 1-403 <HEI>
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A;Status: preliminary
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                                                                                                                                                                                                                                            R;Shigenobu, S.; Watana
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE000833; GB:AE000666; NID:g2621559; PIDN:AAB84999.1; PID:g262156
A;Experimental source: strain Delta H
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                                                              A; Experimental C; Genetics:
                                                                                                     A; Cross-references:
                                                                                                                                                               A;Status:
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                                                                                                                                                                                                   A; Reference number: A84930;
                                                                                                                                                                                                                           A; Title: Genome
                                                                                                                        A;Residues: 1-213 <STO>
                                                                                                                                           A; Molecule type: DNA
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Best Local S
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  ly: orotate phosphoribosyltransferase; orotate phosphoribosyltransferase glycosyltransferase; pentosyltransferase
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source:
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                                                                                3:AP000398; G
: strain APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.5%;
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                                                                                                                                                                                                       the endocellular bacterial symbiont MUID:20445173; PMID:10993077
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                                                                                                   GSPDB:GN00144
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39;
Pred. No.
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probable high-affinity branched-chain amino acid transport ATP-binding protein C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #semiesno vonit.
RESULT
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C;Superfamily: :
F;9-205/Domain:
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A;Accession: F72604
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                                                                                                                                                                                                                                                                                                                            A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80292.1; PID:d1044078; PID:g510
A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-248 < KAW >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Sep-2000
C;Accession: F72604
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A;Cross-references: GB:BA000019; PIDN:BAB75020.1; PID:g17132416;
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G;Accession: AB2221
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi R;Kaneko, T.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2221
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Best Local S
Matches 6
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Best Local (
                                                                                                                                                                                                                                           Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology; 9-205/Domain: ATP-binding cassette homology <ABC>
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Best Local
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                                                                                                                      EKNSFECILGP 12
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                                                                                                                                                               Conservative
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                                                                                                                                                                                  Score 39; DB 2;
Pred. No. 15;
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Pred. No. 14;
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Pred. No. 13;
                                                                                                                                                                 Mismatches
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A;Molecule type: DNA
A;Residues: 2505-2551,'QQQQ',2552-2576,'E',2578-2604 <TAU>
A;Residues: 2505-2551,'QQQQ',2552-2576,'E',2578-2604 <TAU>
R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A;Title: opa: a novel family of transcribed repeats shared by the Notch
A;Reference number: A05267; MUID:85099329; PMID:2981631
A;Accession: A05267
                                                                                                                                                                                          A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C;Superfamily: notch protein; ankyrin repeat homology; BGF homology
C;Keywords: differentiation; tandem repeat; transmembrane protein
F;27-43/Domain: transmembrane #status predicted <TMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Tautz, D.
Nucleic Acids Res. 17, 6463-6471, 1989
Nucleic Acids Res. 17, 6463-6471, 1989
A;Title: Hypervariability of simple sequences as a general source for polymorphic A;Reference number: S09358; MUID:89385974; PMID:2780284
F;297-328/Domain: EGF homology <EGX1>
F;530-561/Domain: EGF homology <EGF1>
F;568-599/Domain: EGF homology <EGF2>
F;988-1019/Domain: EGF homology <EGX2>
F;1064-1095/Domain: EGF homology <EGF3>
F;1187-1218/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 2504-2576,'E',2578-2611 <WHA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-48,'1',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958
A; Residues: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A24768; MUID:86079539; PMID:3935325
A;Accession: A24768
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A;Residues: 1-2703 <KID>
A;Residues: 1-2703 <KID>
A;Cross-references: GB:KO3508; NID:g157991; PIDN:AAA28725.1; PID:g157993
R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
Cell 43, 567-581, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A24420; A24768; S09358; A05267 R;Kidd, S.; Kelley, M.R.; Young, M.W. Mol. Cell. Biol. 6, 3094-3108, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 notch protein - fruit fly (Drosophila melanogaster) N_fAlternate names: neurogenic repetitive locus prot C_fSpecies: Drosophila melanogaster
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A24420
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A;Title: Identification and localization of a sea urchin Notch homologue: insights into A;Reference number: 220966; MUID:97454256; PMID:9310331
A;Accession: T31070
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T31070
R;Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: FlyBase: FBgn0004647
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: notch; opa
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A;Residues: 1-2531 <SHE>
A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A24420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
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Best Local Similarity
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66.7%;
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A;Cross-references: GB:AB001610; GB:AE001363; NID:g4376515; PIDN:AAD18396.1; PID:g437651
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                      R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: C86521
                                                                                                                                                                                                                                                hypothetical protein CPj0243 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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F;1950-1982/Domain: ankyrin repeat homology <AN1>
F;1983-2015/Domain: ankyrin repeat homology <AN2>
F;1988-2004/Domain: transmembrane #status predicted <TMM3>
F;2017-2049/Domain: ankyrin repeat homology <AN3>
F;2050-2082/Domain: ankyrin repeat homology <AN4>
F;2083-2115/Domain: ankyrin repeat homology <AN5>
F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted
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                                   A; Molecule type: DNA
A; Residues: 1-141 <S'
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                                                                                  A;Status: preliminary
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A;Residues: 1-141 <REA>
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                                                                                                                                                                                                                               Accession: C8652
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;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000;Accession: G73100; H81567
Residues: 1-141 <STO>
Cross-references: GB:BA000008; NID:g8978616; PIDN:BAA98453.1; GSPDB:GN00142
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Pred. No. 1.7e
3; Mismatches
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Pred. No. 13;
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                                                                                                      Search completed: March 22, Job time : 2.78043 secs
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A;Molecule type: DNA
A;Residues: 1-306 <AFO>
A;Cross-references: EMBL
C;Genetics:
A;Note: MSV227
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ORF MSV227
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C;Genetics:
A;Gene: CPj0243
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                                                                                                                                                                                                                                      probable DNA-binding regulator protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A;Experimental source: strain A3(2)
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1; Mismatches
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Copyright (c) 1993 - 2004 Compugen Ltd.
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P70708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                           2 anabaena sp
3 strongyloce
5 homo sapien
8 rattus norv
0 arabidopsis
7 lycopersico
0 mus musculu
                                                                                                                                                                               1 arabidopsis
6 rattus norv
8 helicobacte
3 helicobacte
4 homo magculu
6 mus musculu
6 mus musculu
1 mus musculu
1 mus musculu
1 caenorhabdi
8 homo sapien
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5 mus musculu
5 homo sapien
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5 homo sapien
8 mus musculu
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9 campylobact
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7 drosophila
9 agrobacteri
7 brachydanio
0 arabidopsis
                                                                                                                                                        neurospora
bacteroides
    leptospira
klebsiella
                                  rattus norv
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## ALIGNMENTS

Matches

6

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                  RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazel M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazel M.D., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Přannkoch C., Baldwin D., RA Ballew R.M., Besu A., Bexandale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Besu A., Bouck J., Brokstein P., Botshakov S., RA Ballew R.M., Benos P.V., Berman B.P., Shandari D., Bolshakov S., RA Burtis K.C., Besand D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Gelbart W.M., Glasser K., RA Googe F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K., RA Hostin D., Houston K., A., Howland T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K., Alland T.J., Wei M.-H., Ibegwam C., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A., RA Liuk Y., Howlstoy B.C., Mays A., Li J.H., Li Z., Liang Y., Lin X., RA Liuk Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., RA Liuk Y., Howlstoy B.C., Pan S., Polley M., Merbon D.L., Rese M.G., Markulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzpy D.M., Nelson D.L., Ra Ra Lie K.C., Pan S., Pan S., Polley R., Smith T., Shenham M., Stoppa R., Sichelar F., Shen H., Ra Nather B., Wang S.,
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TC_DROME STANDARD; PRT; 2703 AA.
NOTC_DROME STANDARD; PRT; 2703 AA.
P07207; 097458; P04154; Q9W4T8;
01-NOV-1986 (Rel. 03, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neurogenic locus Notch protein precursor.
N OR EG:140G11.1 OR EG:163A10.2 OR CG3936.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence of the notch locus of Drosophila me of the encoded protein to mammalian clotting Mol. Cell. Biol. 6:3094-3108(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
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ng and growth factors.";
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Beinert N., Dowe G., Sc
Callister D.M., Campbel
McMillan P.J., Salles C
Glover D.M.;
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Benos P.V., Gatt M.K., Ashburner M., Brun C., Demailles J., Cadieu E
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Codieu E
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
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Kelley M.R., Kidd S., Berg R.L., Young M.W.;
"Restriction of P-element insertions at the :
melanogaster.";
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                                                                                               "Neurogenic phenotypes a Presenilin mutants.";
Nature 398:525-529(1999)
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Matsuno K., Diederich R.J., Go M.J.,
Artavanis-Tsakonas S.;
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"opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in D. melanogaster.";
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          MEDLINE=21657146; PubMed=1179906
Lieber T., Kidd S., Young M.W.;
"kuzbanian-mediated cleavage of
Genes Dev. 16:209-221(2002).
                                                                                                                                                                                                     Drosophila.";
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MEDLINE=94215489; PubMed=8162848;
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                                                                                                                                                                                                                                                                                                          "Deltex acts as a positive regulator interactions with the Notch ankyrin r Development 121:2633-2644(1995).
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                                                     PubMed=11799064;
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                         Drosophila Notch.";
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repeats.";
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EMBL; M16149; AAB59220.1; JOINED.
EMBL; M16150; AAB59220.1; JOINED.
EMBL; M16151; AAB59220.1; JOINED.
EMBL; K03503; AAA28725.1; JOINED.
EMBL; K03507; AAA28725.1; JOINED.
EMBL; K03507; AAA28725.1; JOINED.
EMBL; K03507; AAA28725.1; JOINED.
EMBL; AL003436; AAF45848.2; —
EMBL; AL0035436; CAB37610.1; —
EMBL; AL0035436; CAB37610.1; JOINED.
EMBL; AL003545; CAB37610.1; JOINED.
EMBL; AL003595; CAB37610.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the NOTCH family.
SIMILARITY: Contains 36 EGP-like domains
SIMILARITY: Contains 3 Lin/Notch repeats
SIMILARITY: Contains 6 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Signaling protein, which regulates, with both positive and negative signals, the differentiation of at least central and peripheral nervous system and eye, wing disk, oogenesis, segmental appendages such as antennae and legs, and muscles, through lateral inhibition or induction. Functions as a receptor for membrane-bound ligands Delta and Serrate to regulate cell-fate determination. Upon ligand activation, and releasing from the cell membrane, the Notch intracellular domain (NICD) forms a transcriptional activates genes of the E(spl) complex. Essential for proper differentiation of ectoderm.

SUBUNIT: Interacts with Su(H) when activated. Interacts with Dx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              via its ANK repeats.

SUBCELLULAR LOCATION: Type I membrane protein. Upon activation SICEALULAR LOCATION: Type I membrane protein. Upon activation SI cleavage, it is released from the cell membrane and enters the nucleus in conjunction with Su(H).

PTM: Upon binding its ligands such as Delta or Serrate, it is cleaved (S2 cleavage) in its such as Delta domain, close to the transmembrane domain. S2 cleavage is probably mediated by Kuz is then cleaved (S3 cleavage) downstream of its transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain, releasing it from the cell membrane.
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                                                                                                                                           M16025;
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                                DEKNSFECILGP 12
DDVNSFKCLCDP
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28-FEB-2003 (Rel. 41, Last sequence up
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Conjugal transfer protein trak.
TRAM OR ATUG127 OR AGR_FTI_237.
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Q44349;
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Pfam; PF03389; Moba MobL; 1.
Conjugation; ATP-binding; Plasmid;
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                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294.2323.2328 (2011). - I- SIMILARITY: Belongs to the mobA/mobL family.
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                                                                                                                                                     PIR; AE3243; AE3243.
PIR; T03419; T03419.
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EMBL; AE009431;
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MEDLINE=21608550; 1
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AE007939; AAK91091.1;
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Score 38; DB Pred. No. 38; 3; Mismatches
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PROSITE; PS00010; ASX HYDROXYL; 9
PROSITE; PS00022; EGF 1; 16.
PROSITE; PS01186; EGF 2; 12.
PROSITE; PS50026; EGF 3; 15.
PROSITE; PS50187; EGF CA; 8.
Calcium-binding; EGF-like domain;
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InterPro; IPR000152; Asx hydroxy1_S.
InterPro; IPR001774; DSL hydroxy1_S.
InterPro; IPR001774; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001438; EGF II.
InterPro; IPR002049; EGF like.
InterPro; IPR002049; Laminin EGF.
InterPro; IPR0030107; VWF_C.
                                                                                                                                                                                          Pfam; PF01414; DSL; 1.

Pfam; PF00008; EGF; 14.

PRINTS; PR00011; EGFLAMININ.

PRINTS; PR00011; EGFLAMININ.

SMART; SM00051; DSL; 1.

SMART; SM00179; EGF CA; 9.

SMART; SM00174; VWC; 1.
                                                                                                                         SMART; SM00179; EGF
SMART; SM00214; VWC
PROSITE; PS00010; A
PROSITE; PS00022; E
PROSITE; PS01186; E
PROSITE; PS50026; E
PROSITE; PS501187; E
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28-FEB-2003
Jagged 1 pre
JAG1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitted (JAN-2000) to the EMBL/GenBank/DDBJ data FUNCTION: Ligand for multiple Notch receptors mediation of Notch signaling (By similarity). in cell-fate decisions.

SUBCELLULAR LOCATION: Type I membrane protein SIMILARITY: Contains 17 EGF-like domains.

SIMILARITY: Contains 1 DSL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                   AF229448; I
ZDB-GENE-01
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                                                                                                 Transmembrane;
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003 (Rel. 41, Last sequence up
003 (Rel. 41, Last annotation
precursor (Jaggedl).
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  DSL.
EGF-LIKE 1.
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EXTRACELLULAR (POTENTIAL POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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tors and involved in the ty). Seems to be involved
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50.0%;
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EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5, CALCIUM
EGF-LIKE 6, CALCIUM
EGF-LIKE 7, CALCIUM
EGF-LIKE 10.
EGF-LIKE 11.
EGF-LIKE 11.
EGF-LIKE 11.
EGF-LIKE 12.
EGF-LIKE 13.
EGF-LIKE 15.
EGF-LIKE 17.

       Score
Pred.
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       38;
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43;
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Q42540; Q8RXQ3;
10-OCT-2003 (Re
10-OCT-2003 (Re
                                                                                                                                                                                                    genome.";
Science 3
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Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence features of the rephysically assigned P1 and DNA Res. 5:379-391(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 42, Last sequence update)
Ubiquitin-conjugating enzyme E2 7 (EC 6.3.2.19) (Ubiquitin-protein ligase 7) (Ubiquitin carrier protein 7).
UBC7 OR ATSG59300 OR MNC17.21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. VIII. Sequence features of the regions of 1,081,958 bp covered by seven physically assigned pland TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Columbia;
MEDLINE=99156233; PubMed=10048488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van Nocker S., Walker J.M., Vierstra R.D.;
"The Arabidopsis thaliana UBC7/13/14 genes
multiubiquitin chain-forming E2 enzymes.";
J. Biol. Chem. 271:12150-12158(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND FUNCTION.
STRAIN-cv. Columbia; TISSUE-Seedling;
MEDLINE-9621824; PubMed-8647807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22954850; PubMed=14593172;
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                                                                FUNCTION: Catalyzes the covalent attachment of ubiquitin to othe proteins so as to signal them for selective protein degradation. Involved in the formation of multiubiquitin chains.

CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP + diphosphate + protein N-ubiquityllysine.

PATHWAY: Ubiquitin conjugation; second step.

MISCELLANGEOUS: A cysteine residue is required for ubiquitin-thiolester formation (By similarity).

SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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A Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
A Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
A Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
A De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
A Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter F.,
A Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter F.,
A Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter F.,
A Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter F.,
A Wincker P., Cattolico L., Weissenbach J., Bangert S.,
A Windelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
A Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
A Wiedelmann R., Kranz H., Voss H., Toppo S., Simionati B.,
A Wezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
A Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
A Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
A Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
A Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
A Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
A Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
A Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
A Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
A Mannhaupt G., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
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Pfam; PP00179; UQ_conjugat; 1.
ProDom; PD000461; UBCc; 1.
SWART; SM00212; UBCc; 1.
SWART; SM00212; UBCQUITIN_CONJUGAT_1; 1.
PROSITE; PS00183; UBIQUITIN_CONJUGAT_2; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
UBIQUITIN_GONJUGAT_2; 1.
UBI CONJUGAT_2; 1.
UBI CONJUGAT_3; UBIQUITIN (BY SIMILARITY)
RTNDING 8 89 UBIQUITIN (BY SIMILARITY)
RTNDING 1-7 ** 18722 MW; 967EF672ADBD6891 CRC64;
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Q42541;
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ubiquitin-conjugating enzyme E2 13 (EC 6.3.2.19) (Ubiquitin-protein ligase 13) (Ubiquitin carrier protein 13).
UBC13 OR AT364640 OR F18L15.180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiubiquitin chain-forming E2 enzymes.";
J. Biol. Chem. 271:12150-12158(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; AB016890; BAB09775.1;
EMBL; AX0080733; AAL86003.1;
EMBL; BT005798; AAC64200.1;
PIR; S71209; S71209.
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MEDLINE=21016720; PubMed=11130713;
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Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Ka Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Lee J.M., Toriumi M.J.,
Ka Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Ka Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
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A Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
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A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                              Query Match
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Matches
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REMBL; AY094040; AAK91385.1; -.

REMBL; AX094040; AAK91385.1; -.

REMBL; AX094040, AAK91385.1; -.

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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome.";
Science 302:842-846(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U33758; AAC49322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- FUNCTION: Catalyzes the covalent attachment of ubiquitin to other proteins so as to signal them for selective protein degradation. Involved in the formation of multiubiquitin chains.
-I- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22954850; PubMed=14593172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diphosphate + protein N-ubiquityllysine.

PATHWAY: Ubiquitin conjugation; second step.

MISCELLANGUUS: A cysteine residue is required for ubiquitin-
thiolester formation (By similarity).

SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                              Similarity 9; Conser
   DEKNIFEWSVTIIGP
                                                             DEKNSFE---CILGP
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Pred. No. 6.6;
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01-FEB-1994
01-FEB-1994
                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-hydroxythreonine-4-phosphate dehydrogenase
                                                                                                                                      PDXA_HELPJ
Q9ZJZ8;
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STRAIN=Sprague-Dawley; TISSUE=Bra
MEDLINE=92210533; PubMed=1313420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RB13
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ras-related protein RAB13.
                     (phosphohydroxy)-L-threonine PDXA OR JHP1490.
Helicobacter pylori J99 (Camp
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PRINTS; PR00449; RAS;
SMART; SM00175; RAB;
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HSSP; P05713; 3RAB.
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InterPro; IPR001806; Ras_trnsfrmng.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           brain and spinal cord.
SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurotransmitter release. TISSUE SPECIFICITY: Highest levels found in lung,
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                                                                                                                                                                                                                                                                                                                                  154
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    Proteobacteria;
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(Rel. 42, Last
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Campylobacter pylori J99).
Epsilonproteobacteria; Campylobacterales;
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GTP (BY SIMILARITY).
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S-geranylgeranyl cysteine
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28-FEB-2003
28-FEB-2003
28-FEB-2003
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
4-hydroxythreonine-4-phosphate dehydrogenase
(phosphohydroxy)-L-threonine dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HELPY
SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
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Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Iv
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
                                                                                                                                                                                                                                     Helicobacter pylori (Campylobacter Bacteria; Proteobacteria; Epsilonpr Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence comparison of two unrelated isolates of the gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyridoxine
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00536; -; 1
InterPro; IPR005255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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NCBI_TaxID=85963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (phosphohydroxy)-L-threonine (HTP) into 2-amino-3-oxo-4-(phosphohydroxy) butyric acid which spontaneously decarboxy form 1-amino-3-(phosphohydroxy) propan-2-one (3-amino-2-oxo) phosphate) (By similarity).

CATALYTIC ACTIVITY: 4-(phosphonooxy)-threonine + NAD(+) = amino-3-oxo-4-phosphonooxybutyrate + NADH.

PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and pyridoxal phosphate.

SIMILARITY: Belongs to the pdxA family.
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                                                                                                                                                                                                                                                                                                                  OR HP1583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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-<; PdxA.
                                                                                                                                                                                                                        cteria; Epsilonproteobacteria;
Helicobacter.
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85.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reductase; NAD; Complete proteome.
77C5FD2DD9A71A81 CRC64;
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TRBM HUMAN
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Matches
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P07204;
01-APR-1986
01-FEB-1991
15-MAR-2004
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HAMAP, MF 00536; -; 1.

InterPro; IPR005255; PdxA.

Pfam; PF04166; PdxA; 1.

TIGR00557; pdxA; 1.

TIGRPAMS; TIGR00557; pdxA; 1.

SEQUENCE 307 AA; 33578 MW; B122B0A0BB00D70E CRC64;
SEQUENCE FROM N.A. MEDLINE=88024950; Wen D., Dittman W.
                                                                                                                                                                                                                             THBD OR THRM.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                        activation.";
EMBO J. 6:1891-1897(1987).
                                                                                              MEDLINE=88004395; PubMed=2820710;
Suzuki K., Kusumoto H., Deyashiki Y., Nishioka
Zushi M., Kawahara S., Honda G., Yamamoto S., I
"Structure and expression of human thrombomodul
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                         Thrombomodulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000655; AAD08621.1;
PIR; G64717; G64717.
TIGR; HP1583; -
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Nature 388:539-547(1997).
                                                                                    receptor on endothelium
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.; "The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Catalyzes the NAD-dependent oxidation of 4-
(phosphohydroxy)-L-threonine (HTP) into 2-amino-3-oxo-4-
(phosphohydroxy) butyric acid which spontaneously decarboxylate
form 1-amino-3-(phosphohydroxy) propan-2-one (3-amino-2-oxopropy
phosphate) (By similarity).

CATALYTIC ACTIVITY: 4-(phosphonooxy)-threonine + NAD(+) = 2-
amino-3-oxo-4-phosphonooxybutyrate + NADH.

PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and
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SUBCELLULAR LOCATION: Cytoplasmic
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4 (Rel. 43,
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PubMed=2822087;
.A., Ye R.D., Deaven
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85.7%;
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                                                                                    cofactor for
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L.L.,
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RA Deloukas P. Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Clington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howlor S.R.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.R.,
RA Milne S.A., Mastry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mastry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mastry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Milnes B.J., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA ROSers J.., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
        Extrausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human thromb localization Biochemistry
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                          Nature
[7]
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Deyashiki Y., Maruyama I., Suzuki K.;
"Gene structure of human thrombomodulin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88227901;
Shirai T., Shioji:
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                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257;
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thrombomodulin gene is intron
cDNA and gene predict protein
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; Poel C.L., Toth
d (MAR-2002) to ti
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m. 103:281-285(1988).
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26:4350-4357(1987).
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1(2001).
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ri S., Ito H., Yamamoto
uyama I., Suzuki K.;
                                                                                                                                                                                                                                                                                                                   PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .Z., Carrington D.P., Chung M.-W., Toth E.J., Yi Q., Nickerson D.A.; to the EMBL/GenBank/DDBJ database
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MEDLINE=58111115; PubMed=7811900;
Oehlin A.-K., Marlar R.A.;
The first mutation identified in the thrombomound of the components of the components of the composition of the components of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sampoli Benitez B.A., Hunter M.J., Meininger D. "Structure of the fifth EGF-like domain of thro EGF-like domain with a novel disulfide-bonding J. Mol. Biol. 273:913-926(1997).
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Protein Sci. 5:195-203(1996).
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MEDLINE=95034791
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Meininger D.P., Hu
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Grinnell B.W.
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MEDLINE=94029900; Pul
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Schherch A., Schein J.E., Jones S.J.M., Marra
"Generation and initial analysis of more than
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2
                                                                                                                                                                                                                                                                                                                                                                                                                             45-year-old man presenting Blood 85:330-336(1995).
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MEDLINE=96276211;
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VARIANT THR-43.
MEDLINE=99057299;
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Norlund L., Holm :
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                                                                                                        L., Horm ...
non thrombomodulin
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main of thrombomodulin.";
  4:1683-1695(1995).
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unter M.J., Komi
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PubMed=8216207;
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                                                                                                                                                            Oehlin
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Marra M./
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VARIANT VAL-473.
VARIANT VAL-473.
MEDLINE=21143723;
Wu K.K., Aleksic N
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01-APR-1990
01-APR-1990
16-OCT-2001
     MEDITINE-89008498; PubMed=2844823;
Dittman W.A., Kumada T., Sadler J.E., Majerus P.W.;
"The structure and function of mouse thrombomodulin. Phorbol myristate acetate stimulates degradation and synthesis of thrombomodulin without affecting mRNA levels in hemangioma cell thrombomodulin without affecting mRNA levels in hemangioma cell J. Biol. Chem. 263:15815-15822(1988).

-i- FUNCTION: Thrombomodulin is a specific endothelial cell rethat forms a 1:1 stoichiometric complex with thrombin. This complex is responsible for the conversion of protein Ca activated protein C (protein Ca). Once evolved, protein Ca scissions the activated cofactors of the coagulation mecha
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDILINE=89128454; PubMed=2536925;

Dittman W.A., Majerus P.W.;

"Sequence of a cDNA for mouse thrombomodulin and predicted mouse and human amino acid sequences.";

Nucleic Acids Res. 17:802-802(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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"Mutations in the thromb
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FUNCTION: Thrombomodulin is a specific endoth that forms a 1:1 stoichiometric complex with complex is responsible for the conversion of activated protein C (protein Ca). Once evolve scissions the activated cofactors of the coag factor Va and factor VIIIa, and thereby reductions of the coag factor value.
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- SUBCELLULAR LOCATION: TO TISSUE SPECIFICITY: End
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; MGI:98736; Thbd.
G0:0009790; P:embryonic development;
G0:0007565; P:pregnancy; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombomodulin (By similarity). SIMILARITY: Contains 6 EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S08488;
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b; IPR001881; EGF Ca.
c; IPR0016209; EGF like.
b; IPR001304; Lectin_C.
c; IPR001491; Thrmbomoduln.
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ial cell;
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C TYPE LECTIN 2; 1
EGF 1; FALSE NEG.
EGF 2; 3.
EGF 3; 3.
EGF CA; 2.
Receptor; Blood co
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Q9Z184;
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                                                                                                                                                                                                                                                                         EMBL; AB013849; bm
MGD; MGI:1338891;
                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Epidermis;
MEDLINE=99192810; PubMed=10092850;
Rusd A.A., Ikejiri Y., Ono H., Yon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                            Hydrolase; Calcium-binding; Multigene family.
CA_BIND 504 515 EF-HAND (POTENTI
                                                                                                                                                                                                                                      InterPro; IPR004303; Prot_arg_deim.
Pfam; PF03068; PAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins.
-!- CATALYTIC ACTIVITY: Protein L-arginine + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Terakawa H., Takahara H., Sugawara K.;
"Three types of mouse peptidylarginine deiminase: characterization tissue distribution.";
J. Biochem. 110:661-666(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION,
MEDLINE=92138676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of cDNAs of mouse peptidylarginine deiminase type
I, type III and type IV, and the expression pattern of type I in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       citrulline + NH(3).

COFACTOR: Requires calcium ions.

TISSUE SPECIFICITY: Epidermis and hair follicles.

SIMILARITY: Belongs to the protein arginine deiminase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Catalyzes the
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                                                                               Similarity
5; Conserv
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(Rel. 39, Last sequence update)
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(Rel. 43, East annotation update)
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75099 MW;
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Sciurognathi; Muridae;
                                                                                                                                                                     BB005AE930AE6F31
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GO; GO:0005112; F:NOtch binding; IDA.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR001774; ESF_2.
InterPro; IPR001774; ESF_Ca.
InterPro; IPR001881; ESF_Ca.
InterPro; IPR001881; ESF_Ti.
InterPro; IPR001438; ESF_1ike.
InterPro; IPR006209; ESF_1ike.
InterPro; IPR006209; ESF_1ike.
InterPro; IPR006209; Taminin_ESF.
pfam; PF01414; DSL; 1.
pfam; PF00010; ESFELOOD.
pRINTS; PR00010; ESFELOOD.
pRINTS; PR00011; ESFELMMININ.
SMART; SM00051; DSL; 1.
SMART; SM00051; DSL; 1.
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
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                  EMBL; AF253469; AAF76428.1;
EMBL; AF273454; AAF78785.1;
EMBL; AB043893; BAB18580.1;
HSSP; P08709; 1BF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shutter J.R., Scully S., Fan W., Richards W.G., Ki Deblandre G.A., Kintner C.R., Stark K.L.; "DI14, a novel Notch ligand expressed in arterial Genes Dev. 14:1313-1318(2000).
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                                                                                                                                    entities requires a license agreement (See http://www.isb-sib
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vasculation
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"A novel Notch ligand
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Yoneya T., Tahara T., Nagao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Adipose tissue;
MEDLINE=20296719; PubMed=10837024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of Delta-4, a new mouse and human Notch ligand.";
J. Biochem. 129:27-34(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane prot
TISSUE SPECIFICITY: Expressed in vascular
SIMILARITY: Contains 8 EGF-like domains.
SIMILARITY: Contains 1 DSL domain.
                                                                                                                                                                                                                                                                                                                                                                                                               Notch-1 and Notch-4.
SUBUNIT: Binds to Notch-1 and Notch-4.
MGI:1859388; D114
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T., Nagao K., Yamada Y.,
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4 precursor (Drosophila Delta
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Sciurognathi; Muridae;
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PS01186;
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(Rel. 42, Last annotation
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6; EGF_2; 7.
6; EGF_3; 8.
e domain; Repeat;
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BY SIMILA
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014578; Q9UPZ7;
30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
28-FEB-2003 (Rel. 4
  This
                                 Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain with large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Connell M., Goela D., Submitted (OCT-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormPep; C34E10.8; CE32158.
Hypothetical protein.
SEQUENCE 1024 AA; 112206
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Mammalia; Eutheria; Primates;
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PIR; T15765; 7
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Submitted (NOV-2002)
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Search completed: March 22, 2004, 06:52:58 Job time: 1.46026 secs
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                                                                                                                     Query Match 55.2%; Score 37; DB 1; Length 1286; Best Local Similarity 75.0%; Pred. No. 68; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                              Coiled coil; PhorbolTester binding; SH3-binding.

NON TER 1 1

DOMĀIN <1 558

DOMAIN 365 561

DOMAIN 509 512

DOMAIN 622 670

DOMAIN 622 670

DOMAIN 702 822

DOMAIN 851 1148

SITE 1212 1217

SEQUENCE 1286 AA; 1146506 MW; 498101F79EA75E85
                                                                                                                                                                                                                                                                                                                                     Pfam; PF00780; CNH; 1.

Pfam; PF00130; DAG PE-bind; 1.

Pfam; PF00169; PH; 1.

SMART; SM00109; C1; 1.

SMART; SM00109; CNH; 1.

SMART; SM00233; PH; 1.

SMART; SM00233; PH; 1.

PROSITE; PS00479; DAG PE BIND DOM 1; 1.

PROSITE; PS0081; DAG PE BIND DOM 2; 1.

PROSITE; PS00081; DAG PE BIND DOM 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:1985; CIT.

MIM; 605629; -.

InterPro; IPR001180; Citron.

InterPro; IPR002219; DAG PE-bind.

InterPro; IPR001849; PH.

InterPro; IPR000861; REM_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AB023166; BAA76793.1; -.
                                                             326 DEKSOFEC 333
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RHO/RAC BINDING.

POLY-LYS.

PHORBOL-ESTER AND DAG BINDING.

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Maximum DB
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Perfect score:
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       seq length: 0
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1: sp_archea:*
2: sp_bacteria:*
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               QBxy55 ralstonia s
Q9yud0 beak and fe
Q8mmm0 corynebacte
Q8dvp3 streptococc
Q87j11 vibrio para
Q9kly9 vibrio chol
Q7uh40 rhodopirell
Q7uh40 rhodopirell
Q26593 methanobact
                                                                                                                                           Q89q37 bradyrhizob
Q9pr76 ureaplasma
Q56605 vibrio chol
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O17727 caenorhabdi
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Q9txx2 caenorhabdi
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Matches 12; Conserv
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Q9U6R7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
98kDa HDM allergen.
Dermatophagoides farinae (House-dust mite).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Pyroglyphidae; Dermatophagoides.
                                                               Weber E.R., Hunter S., Stedman K., McCall C.; "Cloning and Characterization of a 98 kDa Allergen from
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Weber E.R., Hunter S.,
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6954;
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 Score 67; DB 5;
Pred. No. 0.00025;
Mismatches 0;
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                               Length 555;
   Indels
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OByrcf6 aeropyrum p
OTV2U1 prochloroco
OB97f5 clostridium
OD5698 rhizobium 1
P95623 rhizobium 1
O30659 rhizobium 1
O80311 brachydanio
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O54391 microcystis
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O04978 oryza sativ
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Q9yv15 melanoplus
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RESULT 3

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AC 9816

AC 9816

DT 91--

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2001) to the ENEL; AR106577; AAC78194.1; -. PIK; F88028; F88028; WormPep; F46F5.15; CE19431. Hypothetical protein. SEQUENCE 180 AA; 20139 MW;
                                                                                                                                                                                                                                                                                                                                                                                          Q81G84;
Q81G84;
01-JUN-2003
01-JUN-2003
01-OCT-2003
                    SEQUENCE FROM N.A.
MEDINE=22608415; PubMed=12721630;
MEDINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., G
Kapatral V., Bhattacharyya A., Reznik
Chu L., Mazur M., Goltsman E., Larsen
Chu L., Mazur M., Goltsman E., Larsen
                                                                                                                                                                                                                                                              Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                           2-aminoethylphosphonate
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STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller N., Wamsley P., Twyma
"The sequence of C. elegans
Submitted (NOV-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. investigating biology. The C. elegascience 282:2012-2018(1998).
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Eukaryota; Metazoa; Nematoda;
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80.0%;
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transport ATP-binding prote
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Caenorhabditis.
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EMBL/GenBank/DDBJ databases
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Pred. No.
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Galleron N., Candelon B.,
K.G., Mikhailova N., Lapidus A.,
n.N., D'Souza M., Walunas T.,
Fonstein M., Ehrlich S.D.,
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP-binding; IEA.
GO; GO:0005524; F:ATP-binding cassette (ABC) transg
GO; GO:0004009; F:ATP-binding cassette (ABC) transg
GO; GO:0000166; F:nuclectide binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR00359; AAA ATPase.
InterPro; IPR00359; ABC transporter.
Ffam; PF00005; ABC tran; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00021; ABC TRANSPORTER 1; 1.
PROSITE; PS00021; ABC TRANSPORTER 2; 1.
ATP-binding; Complete protecme.
SEQUENCE 333 AA; 37238 MW; 762C5CB21A582BED CRO
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01-JAN-1998
01-JUN-2003
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Nature 423:87-91(2003)
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                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Nem
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72.7%;
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Pred. No. 4;
2; Mismatches
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Last sequence update)
Last annotation updat
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Best Local
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EMBL; AE002106; AAF30474.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding cassette (ABC)
GO; GO:0004009; F:ATP-binding cassette (ABC)
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of nitrogen-fixing syn Bradyrhizobium japonicum USDA110."; Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).

EMBL; AP005947; BAC48558.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004009; F:ATP-binding (assette (ABC) transport).

GO; GO:0004009; F:ATP-binding cassette (ABC) transport; IEA.

InterPro; IRN03439; ABC_transporter.

Pfam; PF0005; ABC_tran; I.

PROSITE; PS50893; ABC_TRANSPORTER_2; 1.

ATP-binding; Complete proteome.

SEQUENCE 258 AA; 28777 MM; 8FD3D9ADFB2475C7 (
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MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S.,
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Cassell G.H.;
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SEQUENCE
                                     SMART; SM00382; AAA; 1.

PROSITE; PS50893; ABC_TRANSPORTER_1;

PROSITE; PS50893; ABC_TRANSPORTER_2;
                                                                                    ProDom; PD000006; ABC
SMART; SM00382; AAA;
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Pfam; PF00005; ABC tra
                                                                                                                                                                                                                                                                                                                                                                      "The complete sequence of urealyticum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
NCBI_TaxID=134821;
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
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01-OCT-2003
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01-OCT-2000
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Bradyrhizobiaceae; Bradyrhizobium.
MCBI_TaxID=375;
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BLR3293.
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proteome.
291 AA;
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Pred. No.
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Matches 8
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Q8XY55;
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01-MAR-2002
01-MAR-2002
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01-NOV-1996
01-NOV-1996
01-JUN-2003
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SEQUENCE
                                                                                   MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguiter P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
"Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raistonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable signal peptide RSC1908 OR RSC3476.
                                                             EMBL; AL646067; CAD15610.1;
                                                                                                                                                                                                                                                                                                                                                                  STRAIN=GMI1000
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Vibrionaceae; Vibrio.
   Complete proteome.
SEQUENCE 67 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=305;
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MEDLINE=96414469; PubMed=8817490;
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      Submitted (MAY-2004)
EMBL, AP005282; BAB99946.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette
GO; GO:000610; P:transport; IEA.
InterPro; IPR003439; ABC_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8NMMO;
Q8NMMO;
01-OCT-2002
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MEDLINE-99009397; PubMed-9791035;
Bassami M.R., Berryman D., Wilcox G.E., Raidal S.R.;
Bassami m.R. Berryman D., Wilcox G.E., Raidal S.R.;
"Psittacine beak and feather disease virus nucleotide sequence
analysis and its relationship to porcine circovirus, plant
circoviruses, and chicken anaemia virus.";
Virology 249:453-459(1998).
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Submitted (JUL-1998) to the
EMBL; AF080560; AAC69867.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
VARIANT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beak and feather disease virus. Viruses; ssDNA viruses; Circovi
                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                                                                 "Complete genomic sequence of Submitted (MAY-2002) to the EN
                                                                                                                                                                                                                                                                                Nakagawa S.;
                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 13032
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                            DSM 20300 / NCIB 10025;
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, Last sequence upo
, Last annotation v
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e EMBL/GenBank/DDBJ databa
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Pred. No.
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Pred. No.
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1; Mismatches
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AE1BB9AF83B09925
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                                                                                               transporter
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databases.
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                                                                                               acti.
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   RESULT
Q87JL1
Q87JL1
Q0 AC Q8
AC Q8
DT 01
DT 01
DT 01
DT 01
OS VI
OC B8
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Q87JL1; Q87JL1; 01-JUN-2003 01-JUN-2003 01-OCT-2003

PRELIMINARY;

372

B

(TrEMBLrel. 24, C) (TrEMBLrel. 24, L, (TrEMBLrel. 25, L, orter, ATP-binding

Last sequence update)
Last annotation updat

protein.

Created)

Vibrio parahaemolyticus. Bacteria; Proteobacteria;

Gammaproteobacteria; Vibrionales;

ABC transporter, VPA0238.

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                                           Query Match
Best Local S
Matches 8
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Best Local S
Matches 7
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PROSITE; PS50893; P
Complete proteome.
SEQUENCE 236 AA;
                                                                                                                                                                                        Proc. Natl Acad. Sci. U.S.A. 99:14434-
EMBL, AE014889; AAN58183.1; -
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette
GO; GO:0000166; F:nucleotide binding; I
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                              MEDIINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
"Genome sequence of Streptococcus mutans UA159, a cariogenic o
                                                                                                                                                                                                                                                                                                                                                                                                                      Putative ABC transporter, SMU.431.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003
01-OCT-2003
                                                                                                                                Pfam; PF00005; ABC tran;
ProDom; PD000006; ABC tra
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                             STRAIN=UA159 / ATCC 700610 / Serotype MEDLINE=22295063; PubMed=12397186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8DVP3;
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                                                                                      PROSITE; PS00211; ABC_TRANSPORTER_1;
PROSITE; PS50893; ABC_TRANSPORTER_2;
ATP-binding; Complete proteome.
SEQUENCE 289 AA; 32170 MW; C33991
                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus mutans.
                                                                                                                                                                                                                                                                      pathogen.'
                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes;
                                                                                                                                                                  InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
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 27
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7; Conserv
                                           Similarity
8; Conserv
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236 AA;
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 EKGSFTAILGP
                       EKNSFECILGP
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3 (TrEMBLrel. 23, 1
6 (TrEMBLrel. 25, 1
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                                             Conservative
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ABC_TRANSPORTER_2;
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                                                      59.7%;
72.7%;
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 37
                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillales; Streptococcaceae;
                                                                                                                                              transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                           Score 40; DB Pred. No. 21; 0; Mismatches
                                                                                                                                                                                                                                                            99:14434-14439(2002).
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                                                                                         C3399DF9E86A5023 CRC64;
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                                                      DB
21;
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J.J.;
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RESULT
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Best Local S
Matches 7
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InterPro; IPR003439; ABC transporter.
InterPro; IPR008995; MOP-like.
Pfam; PF00005; ABC tran; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
ATP-binding; Complete protecome.
SEQUENCE 372 AA; 41100 MW; 16BBFB0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000
01-OCT-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=El Tor N16961 / Serotype 01;
MEDLINE=20406833; bubmed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO
                                                                                                                                               EMBL;
PIR; H
HSSP;
TIGR;
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MEDLINE=22508454; PubMed=12620739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                         Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KLY9
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NCBI_TaxID=670;
                                                                                                                                                                                                                                                                    - i - SIMILARITY:
                                                                                                                                                                                                                                                                                                                   cholerae.";
                                                                                                                                                                                                                                                                                                                                      "DNA sequence of both chromosomes of
                                                                                                                                                                                                                                                                                                                                                                 Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae
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GO:0016020; C:membrane; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0004009; F:ATP-binding cassette (AB(GO:0000166; F:nucleotide binding; IEA.
GO:0000166; P:transport; IEA.
GO:0006810; P:transport; IEA.
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GO:0016020; C:membrane; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0004009; F:ATP-binding cassette
GO:0006810; P:transport; IEA.
                                                                                                                                                                                          ; AE004390; AAF96503.1;
H82440; H82440.
                                                                                                                                                                                                                                         (ABC TRANSPORTERS)
                                                                                                                                               Q58663; 1G6H.
VCA0602; -.
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Matches 8
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PROSITE; PS50893; ABC TRANSPORTER 2; 1.

ATP-binding; Transport; Complete proteome.

SEQUENCE 403 AA; 44956 MW; 887B28C76EA26272
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee Aldredge T., Bashirzadeh R., Blakely D., Cook R., Charlson D., Hoang L., Keagle P., Lumm W., Pothier
                                                                                                                                                                                                                                                                                                                                          Hypothetical MTH493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; SEQUENCE 455 AA; 4
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Planctomycetaceae; Pirellula.
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                                                                                          STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                            Methanobacterium thermoautotrophicum. Archaea; Euryarchaeota; Methanobacteria;
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Gloeckner F.O., Kube M., Bauer M., Teelj
Ludwig W., Gade D., Beck A., Borzym K.,
Schlesner H., Amann R., Reinhardt R.;
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                                                                                                                                                           SEQUENCE
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NCBI_TaxID=187420;
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RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RY "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).

DR EMBL, AE000833; AAB84999.1; -.
DR PIR; G69164, G69164.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 187 AA; 20693 MW; D778F23DFAC04032 CRC64;
Cuery Match
Best Local Similarity 54.5%; Score 39; DB 17; Length 187;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QV 1 DEKNSFECILG 11
Db 28 DEHNMIQCVLG 38

Search completed: March 22, 2004, 06:59:16

Job time: 5.41467 secs
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67
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

RESULT 1
AAY52514
ID AAY5 WO9954349-A2 canine; veterinary; antibody; vaccine; immunisation. Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; House dust mite allergen protein (map) A/B fragment map(4). AAY52514; 16-APR-1999; 28-OCT-1999. Dermatophagoides farinae. 22-FEB-2000 (first entry) AAY52514 standard; peptide; 12 AA 99WO-US008524

17-APR-1998; 13-MAY-1998; 02-SEP-1998; 98US-00062013. 98US-0085295P. 98US-0098909P.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber ER;

WPI; 2000-052700/04.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Claim 3; Page 69; 154pp; English.

Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWM map) composition. The HWM-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. The HWM-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines,

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humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins

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AAU96318 standard; peptide; 12

Matches Query Match Best Local

12;

Conservative

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Mismatches

Indels

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Gaps

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DEKNSFECILGP 12 DEKNSFECILGP

12

Similarity

100.0%;

Score 67; DB 3; Pred. No. 4.8e-05;

Length 12;

Sequence 12 AA;

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The invention relates to an isolated mite allergenic protein of CD Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-protein protein protein or a reagent comprising a non-composition is useful for identifying an animal (e.g., dog, CC cat) susceptible to or having an allergic response to a mite. An CC therapeutic composition is useful for desensitising a host animal to an CC dilergic response to a mite. The DNA and protein can be used in the CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting CC disease. Antibodies to 193, to prevent immunocomplex formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 CC represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 70; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mccall CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mate allergenic protein; immunocomplex formation.
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                                                                                                                                                                                                                                                                                                                                                                                                   mite allergenic protein isolated from Dermatophagoides, designa HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hunter SW,
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                                                    This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-536, the mature form of PDerf98-555 (AAX52523). PDerf98-536 has a molecular weight of 98 kD, comprising 53 6 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to Ig3 present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins.
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13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-cross epicope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)s or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 or represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                     AAY52523;
                                                                                               AAY52523 standard; protein; 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 536 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 125-127; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mite allergenic protein isolated from Dermatophagoides, designa Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 5; Length 536; Pred. No. 0.0021;
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RESULT 6
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ID AAU9
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AAU96327 standard; protein; 555

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Matches Query Match Best Local (

l Similarity 12; Conserv

Conservative

0

Mismatches

100.0%;

Score 67; DB 3; Pred. No. 0.0022;

Length 555;

0

Gaps

0

DEKNSFECILGP

DEKNSFECILGP

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homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite
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13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                    This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-55. PDerf98-555 has a molecular weight of 98 kD, comprising 555 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) composition. The HMW-map composition was isolated from a D. farinae high the faller composition was isolated from a D. farinae
Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mite allergen protein; map; high molecular weight; HMM-map; allergy; house dust mite; igE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-052700/04.
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                                                                                                                                                                                                                                                                                                                                                                                                         Page 111-113; 154pp; English
                                 from a mixture of proteins
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98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                          Matches
                            Der HYM-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                     15-JUL-2002
                                                                                                                                                             AAU96328 standard; protein; 555 AA
                                                                                                                                                                                                                                                                                                                                                   Sequence 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Der HMW-map;
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                                                                       HMW-map
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                                                                       polypeptide #15
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Pred. No. 0.0022;
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E; hypersensitivity;
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                                                                                                                                                                                                                                                                                                                      Length 555;
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Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                        Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fel
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                                                                                                                                                                                                                         D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490
                                                                                                                                                                                                                                                         06-AUG-2003
22-FEB-2000
                                                                                                                                                                                                                                                                                                        AAY52535;
                                                                                                                                                                                                                                                                                                                                     AAY52535 standard; protein; 490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 555 AA;
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                                                                                                                                           canine; veterinary; antibody; vaccine; immunisation.
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Pred. No. 0.0022;
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Modified-site

/note= "Asn is N-glycosylated" 240. .242

is N-glycosylated

Location/Qualifiers 115. .117

Modified-site

Dermatophagoides pteronyssinus.

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RESULT 9
AAU96339
ID AAU9
AC AAU9
XX LS-J
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13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490 has a molecular weight of 98 kD, comprising 490 maino acids, and has a high degree of homology with the D. farinae mature 98 kD allergen, mapB (AAY52525). Nucleic acid molecules encoding PDerp98-490 were isolated from a D. pteronyssius cDNA library by hybridisation with a probe encoding the D. farinae high molecular weight map (HMW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them,
                                                                                                                                                                                                                                        Der HMW-map; American house dust mite; antiallergic; mite allergenic protein; immunoglobulin E; hypersens: immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU96339 standard; protein; 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
   14-SEP-2001; 2001WO-US028730
                                                                                                                                                                             Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                              Der HMW-map polypeptide #26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mixture of proteins. (Updated on 06-AUG-2003 to correct OS field
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may be used in therapeutic compositions to modify an animal's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 147-149; 154pp; English.
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                                                                                                                     WO200222807-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEKNSYECLLGP 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEKNSFECILGP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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98US-0085295P.
98US-0098909P.
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Pred. No. 0.01
2; Mismatches
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy, treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                              06-AUG-2003
22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                             AAY52533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its relate acid. The Der HMW-map protein is useful for eliciting an immune against Der HMW-map protein. The protein or a reagent comprising
                                                                                                                                                                                                                                                                                                                             D. pteronyssius 98 kD mite allergen protein (map) PDerp98-509
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY52533 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mite allergenic protein isolated from Dermatophagoides, designated 
Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                            28-OCT-1999
                                                                                                                                        Protein
                                                                                                                                                                                                                    Dermatophagoides pteronyssinus.
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                                                                                          WC9954349-A2
                                                                                                                                                                       Peptide
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(first entry)
                                                                                                                        20. .50
/note=
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                      /note= "Signal peptide"
                                                                                                                                        .509
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83.3%;
                                                                                                                         "Mature PDerp98-509"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its related nucleic
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17-APR-1998;

98US-00062013 99WO-US008524

16-APR-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD, comprising 509 amino acids, and has a high degree of homology with the D. farinae 98 kD allergen, maps (AAYS2523). Nucleic acid molecules encoding PDerp98-509 were isolated from a D. pteronyssius cDNA library by hybridisation with a probe encoding the D. farinae high molecular weight map (HMW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins and peptides can also be used to diagnose allerges via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as recover desired dust mite allergens from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
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Best Local S
Matches 10
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02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Der HWW-map; American house dust mite; antiallergic; mite; l
mite allergenic protein; immunoglobulin E; hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Der HMW-map
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                                Mccall CA,
                                                                                                                                                14-SEP-2000;
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                                                                                                                                                                                                                                                                21-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                          Dermatophagoides
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                                                                                                                                                                                                                                                                                                                                                                                                                                     immunocomplex formation.
                                                                                           (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide #24.
                                Hunter SW,
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                                                                                                                                                2000US-00662293
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98US-0098909P
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                                Weber ER;
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Pred. No. 0.
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RESULT 12
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Der HMW-map polypeptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU96338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU96338 standard; protein; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dermatophagoides farinae
                                                                                          Claim 12; Page 139~141; 161pp; English.
                                                                                                                                                   New mite allergenic protein
Der HMW-map protein, useful
                                                                                                                                                                                                                                                       N-PSDB; ABK69583
                                                                                                                                                                                                                                                                                                                                                     Mccall CA, Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunocomplex formation.
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                                                                                                                                                                                                                                                                                         2002-351888/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEKNSYECLIGP 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                        Weber ER
                                                                                                                                                   isolated from Dermatophagoides, as a vaccine for treating mite
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Pred. No. 0.015;
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                                                                                                                                                          allergy.
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic

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RESULT 13
ABU48773
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Matches 10
The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)S or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
                                                                                                                                                                                                                                                                   Wang
Wall
                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072681.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                            New antisense nucleic acids, useful for identifying for homologous nucleic acids required for cellular p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU48773;
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                                                                                                                                   Claim 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #34300
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Trawick
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                                                                                                                                 SEQ ID NO 76697; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; cell proliferation; drug design
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Forsyth !
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                                                                                                                                                             discovery programs.
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Xu HH;
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RESULT 14
AAG92550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 8
                                                                                                                                                                                                              16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                   Nakagawa
Tateishi
                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                          20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                         EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                   organic
                                                                                                                                                                                                                                                                                                                                                                                                                   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                C glutamicum
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                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium
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                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                       2001-376931/40.
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8; Conserv
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Senoh A, Ikeda
                                                                                                                                                                                                                2000JP-00159162.
2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                     synthesis.
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72.7%;
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da M,
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                                                                                                                                   S, Hayashi M,
Ozaki A;
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Claim 17; SEC ID NO 6304; 246pp + Sequence Listing; English

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RESULT 15
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08-JUL-1999
08-JUL-1999
09-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformatio genome mapping; genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 236
                                                                09-JUL-1999
14-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum.
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99DE-01032128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           fine chemical production; transformation;
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Search completed: March 22, Job time : 5.64869 secs

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31-AUG-1999
03-SEP-1999
03-SEP-1999
                                                                                                                             AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention
                                                                                                      Sequence 284 AA;
                                                                                                                                                                                                                                                                                                                 Corynebacteium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing outdentifying C. glutamicum or related bacteria, and as markers for
                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                         transformation.
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Post-processing: Minimum Match 0%
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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3 6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
5 6/ptodata/2/pubpaa/US08_EW_PUB.pep:*
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Sequence 287, App	Sequence 3, Appli	Sequence 38990, A	-	Sequence 446, App	6304,	Sequence 76697, A	Sequence 16621, A	38,	Sequence 35, Appl	Sequence 41, Appl	18,	15,	21,	Sequence 5, Appli	Description

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## ALIGNMENTS

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TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: AL-2-C3

CURRENT APPLICATION NUMBER: US/10/218,743

CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: US/09/292,225

PRIOR TILING DATE: 1999-04-15

PRIOR APPLICATION NUMBER: 60/098,909

PRIOR APPLICATION NUMBER: 60/098,909

PRIOR APPLICATION NUMBER: 60/098,509

PRIOR PRIOR PILING DATE: 1998-09-02

PRIOR APPLICATION NUMBER: 60/085,295

PRIOR FILING DATE: 1998-09-5-13

PRIOR APPLICATION NUMBER: 60/098,565

PRIOR APPLICATION NUMBER: 60/062,013

PRIOR APPLICATION NUMBER: 60/062,013

PRIOR PILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 49

COCEMBRE OF SEQ ID NOS: 49
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                                                                                                                                                                                                           ; ORGANISM: Dermatophagoides farinae US-10-218-743-5
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US-10-218-743-5
/ Sequence 5, Application US/10218743
/ Publication No. US20030096779A1
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                          LENGTH: 12
TYPE: PRT
                                                               y Match 100.0%; Score 67; DB 14; Length 12; Local Similarity 100.0%; Pred. No. 1.7e-05; hes 12; Conservative 0; Mismatches 0; Indels
DEKNSFECILGP 12
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SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 555
TYPE: PRT
ORGANISM: Dermatophagoides farinae
US-10-218-743-15
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Publication No. US20030096779A1
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APPLICANT: McCall, Catherine A.

APPLICANT: Hunter, Shirley Wu

APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: AL-2-C3
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
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PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3 CURRENT APPLICATION NUMBER: US/10/218,743 CURRENT FILING DATE: 2002-08-13 CURRENT FILING DATE: 2002-08-13
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PRIOR FILING DATE: 1998-04-17
                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/062,013 PRIOR FILING DATE: 1998-04-17
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PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-09-02
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Weber, Eric R.
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D. US20030096779A1
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: WOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-03
PRIOR APPLICATION NUMBER: 60/098,565
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-02
PRIOR PILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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Matches 12
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 18
LENGTH: 555
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Best Local Similarity
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/062,013
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ORGANISM: Dermatophagoides farinae
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                                                                                                                                                                                                                                                                                                                                                            r, Catherine A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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Pred. No. 0.00098;
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Pred. No. 0.00098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 555;
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APPLICATION NUMBER: 09/062,013 FILING DATE: 1998-04-17

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Sequence 38, Application US/10218743

Publication No. US20030096779A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: McDer, Eric R.

TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/9/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-09-02
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                                                                                                                                                                                                                                                                                                                                                      RESULT 7
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR PRIOR PRIOR NUMBER: 60/098,909
PRIOR PRIOR PRIOR DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098,295
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-05-13
PRIOR PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
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US-10-218-743-35
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Best Local Similarity
Matches 10; Conservat
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APPLICANT: MCCall, Catherine A.
APPLICANT: Hunter, Shirley Mu
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 490
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Best Local :
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mes 10; Conserv
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Pred. No. 0.007;
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GENERAL INFORMATION:

APPLICANT: Wang, APPLICANT: Zamuć

Zamudio, Carlo Malone, Cheryl Haselbeck, Robert Ohlsen, Kari Zyskind, Judith

Liangsu Carlos

APPLICANT APPLICANT: PPLICANT

Yamamoto, Robert Forsyth, R. Xu, H. Carr, Grant Trawick, John Wall, Daniel Sequence 76697, Application US/10282122A Publication No. US20040029129A1

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APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
FRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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US-10-282-122A-76697
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SEQ ID NO 38
LENGTH: 509
TYPE: PRT
ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                                    Local Similarity
tes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                       64.2%;
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Pred. No. 11;
1; Mismatches
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Pred. No. 0.0073;
                                                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                          15; Length 258;
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US-09-738-626-6304

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                                                                                                                    FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
                                                     SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 6304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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PRIOR
PRIOR
                                                                                          PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
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CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                        NAPPLICANT: OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
DRGANISM: Corynebacterium glutamicum
                                    ENGTH: 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 KKNSFTTILGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LING DATE: 2000-10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                    YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                     HAYASHI, MIKII
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEIKO
                                                                                                                                                                                                                                                                                                                      MASATO
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72.7%;
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i Mismatches
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RESULT 12 US-10-627-476-450

Sequence 450, Applic Publication No. US20 GENERAL INFORMATION:

Application US/10627476 o. US20040030116A1

APPLICANT: Pompejus, Mark APPLICANT: Kroger, Burkhard APPLICANT: Schoder, Hartwig APPLICANT: Zelder, Oskar

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                                                                                                                                              ; ORGANISM: Corynebacterium glutamicum US-10-627-476-446
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                                                                    Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                 SEQ ID NO 446
LENGTH: 284
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Best Local
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CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 09/602,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931454.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-125CPCN
                                                                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 678
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: DE 19932180.9 PRIOR FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRA
TITLE OF INVENTION: TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                      TYPE: PRT
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932125.6
FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE 19932122.1 FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE 19932128.0
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: DE 19932124.8
                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-07-09
73 EKNKFTAIMGP 83
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7; Conserv
                                  2 EKNSFECILGP 12
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Zelder, Oskar
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                                                                      Conservative
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                                                                                       59.7%;
                                                                      Score 40; DB
Pred. No. 42;
1; Mismatches
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Pred. No.
                                                                                   DB 42;
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Best Local :
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LENGTH: 284
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Patent No. US20020048763A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/602,787
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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CURRENT APPLICATION NUMBER: US/10/627,476
CURRENT FILING DATE: 2003-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFULTILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: DE 19931454.3 PRIOR FILING DATE: 1999-07-08
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G.
                                                                                                  APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
ADDITION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: DE 19932180.9 FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DE 19932125.6 FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: DE 19932124.8 FILING DATE: 1999-07-09
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                                                                                         APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                  APPLICATION NUMBER: GB 24263.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank, David R.
Hanzel, David K.
Chen, Wensheng
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                                                                   2001-01-30
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PCT/US01/00664
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Pred. No.
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42;
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Query Match
Best Local Similarity
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                                                                                                      US-09-838-955-3
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US-09-838-955-3
                                                                                                                                                                               APPLICANT: Kelly, James D
APPLICANT: Melotto, Maeli
TITLE OF INVENTION: DNA Encoding For A Disease Resistance Gene From Common
TITLE OF INVENTION: Bean and Methods of Use
FILE REFERENCE: 6550-000044
CURRENT APPLICATION NUMBER: US/09/838,955
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09838955
Patent No. US20020056152A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38990
LENGTH: 51
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Best Local Similarity
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HELAT, SIGNAL = 13
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BOALM MARROW, SIGNAL = 9
OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 12
OTHER INFORMATION: SWISSPROT HIT: 088807, EVALUE 3.00e-07
OTHER INFORMATION: EXTHUMAN HIT: BE089551.1, EVALUE 2.90e+00
                                                                                                               TYPE: PRT ORGANISM: Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MAP TO OTHER INFORMATION: EXPRESS
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                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00668
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ilarity 54.5%;
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EXPRESSED 1
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                   Score 38; DB 9;
Pred. No. 1.3e+02;
3; Mismatches 2
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                                                         Length 369;
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Db 162 KRSIFHCILGP 172

RESULT 15
US-10-363-493-287
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US-10-365-493-287
US-10-365-493-287
US-10-365-493-287
US-10-365-493-287
US-10-365-493-287

SEQUENCE 287, Application US/10369493
PLICANT: Colonar, Barry S.
APPLICANT: Colonar, Barry S.
APPLICANT: Goldman, Barry S.
CURRENT PILLING DATE: 2000-02-28

PRIOR FILLING DATE: 2000-02-21

NOWBER OF SEQ ID NOS: 47374

SEQ ID NO 287

CURRENT PILLING DATE: 2000-02-21

CURRENT PILLING DATE: 2000-02-21

CURRENT PILLING DATE: 2000-02-21

SECURIAN SEC
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Minimum
Maximum
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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67
1 DEKNSFECILGP 1:
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Match Length
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      Issued_Patents_AA:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-918-723-4
US-08-918-723-4
US-08-918-723-7
US-08-12-870-9
US-08-12-870-9
US-08-312-870-9
US-08-312-870-9
US-08-312-870-9
US-08-312-870-9
US-08-312-870-9
US-08-312-870-9
US-08-389-3
US-08-389-3
US-08-387-389-3
US-08-387-344A-1
US-08-387-389-3
US-08-587-389-2
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538, Appl
538, Appl
19, Appl
129, Appl
13, Appl
14, Appl
15, Appl
16, Appl
16, Appl
17, Appl
18, Appl
18, Appl
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US-09-880-484D-2	US-08-170-290A-54	US-08-312-870-1	US-08-261-206A-59	5256770-7	US-08-733-564-2	US-09-331-793-4	US-08-312-870-3	US-08-110-011A-16	US-08-110-011A-14	US-08-014-723-16	US-08-014-723-14	US-08-110-011A-18	US-08-110-011A-2	US-08-110-011A-1	US-08-014-723-18	US-08-014-723-2	US-08-014-723-1
Sequence 2, Appli	Sequence 54, Appl	Sequence 1, Appli	Sequence 59, Appl	ຫຼ	Sequence 2, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 16, Appl	~	•	Sequence 14, Appl	Sequence 18, Appl	Sequence 2, Appli	Sequence 1, Appli		•	Sequence 1, Appli

## ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
CURLENT OF INVENTION: NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-03
EARLIER FILING DATE: 1998-09-05
EARLIER FILING DATE: 1998-09-05
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER PILING DATE: 1998-04-17
SARTHER PILING DATE: 1998-04-17
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US-09-292-225-21
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US-09-292-225-5
                      Sequence 21, Application US/09292225
PATENT NO. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: ALL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
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CURRENT APPLICATION NUMBER: US/09/292,225
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ilarity 100.0%;
Conservative 0
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                                                                                         ACID MOLECULES,
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RESULT 4
US-09-292-225-18
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US-09-292-225-15
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; SEQ ID NO 21
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
NUMBER: OF SEQ ID NOS: 49
NUMBER: OF SEQ ID NOS: 49
NUMBER: OF SEQ ID NOS: 49
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
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Best Local S
Matches 12
Sequence 18, Application US/09292225
PATENT NO. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPH
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 555
TYPE: PRT
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Patent No. 6455686
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Dermatophagoides farinae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF
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    NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
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100.0%; Pred. No. 0.0006;
tive 0; Mismatches 0
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Pred. No. 0.00058;
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RESULT 6 US-09-292-225-35

Sequence 35, Application US/09292225 Patent No. 6455686 GENERRAL INFORMATION: APPLICANT: McCall, Catherine A.

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; SEQ ID NO 41
, LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-41
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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US-09-292-225-41
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-18
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-05
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MCCAll, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
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                                                                                                   Query Match
Best Local (
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Best Local
                                                                                Matches
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EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
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385
285
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                                       1 DEKNSFECILGP 12
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DEKNSYECLIGP 396
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100.0%; Pr
                                                                                                   92.5%;
83.3%;
                                                                                                   Pred. No.
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Pred. No. 0.0006;
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RESULT 8
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; Sequence 5794, Application US/09328352
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-05
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 38
LENGTH: 509
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Best Local Similarity
Matches 10; Conser
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SEQ ID NO 35
LENGTH: 509
TYPE: PRT
ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Dermatophagoides farinae
09-292-225-38
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Patent No. 645568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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CURRENT FILING DATE: 1999-04-15
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APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 0.0042;
2; Mismatches
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Pred. No. 0.0042;
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APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5794
LENGTH: 118
TYPE: PRT
GRANISM: Acinetobacter baumannii
US-09-328-352-5794
Query Match
Best Local Similarity
'ntches 6; Conserve
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COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Matches 6; Conserv
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                                                                                                                                                                  TELEFAX: (212) 869-8864/9
TELEX: 66141 PENNIE
TINFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 2703 amino acids
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APPLICANT:
APPLICANT:
                                                                                                                MOLECULE TYPE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
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TELEPAX: (212) 869-8864/9741
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                                                                                                                                                amino acid
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1155 Avenue of the Americas
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                                                                                                              protein
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Pred. No.
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Conservative

50.0%;

Score 39; DB 1; Pred. No. 2.6e+02;

Length 2703;

Mismatches

Indels

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Gaps

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Query Match
Best Local Similarity
Tatches 6; Conserve
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US-08-899-232-4
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                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA ENCODING FOR A DISEASE RESISTANCE GENE FROM COMMON BEAN AND TITLE OF INVENTION: OF USE FILE REFERENCE: 6550-000044 CURRENT APPLICATION NUMBER: US/09/838,955A CURRENT FILING DATE: 2003-02-24 NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin version 3.1 SEQ ID NO 3
                                                                                        Sequence 129, Application US/08927219
Patent No. 6187533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Patent No. 6646183
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Best Local Similarity
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Patent No. 6436650
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CURRENT FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Qi, Huilin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kelly, o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Michigan State University APPLICANT: Kelly, James D
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TYPE: PRT
ORGANISM: Drosophila sp.
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 369
                              APPLICANT:
 APPLICANT:
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            Yamagata, Kazuya
Oda, Naohisha
Kaisaki, Pamela J.
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Furuta, Hiroto
                                                           Bell, Graeme I.
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54.5%;
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Pred. No. 2.6e-
3; Mismatches
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Pred. No.
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2.6e+02;
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RESULT 13
US-08-918-723-4
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Patent No. 586377
GENERAL INFORMAT
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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acid
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APPLICATION NUMBER: US 60/
FILING DATE: 02-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                           APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: UBC7-LIKE UBIQUITIN-CONJUGATING ENZYME
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                 CORRESPONDENCE ADDRESS
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STREET: 51.
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FILING DATE: Concurrently Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                           381 NAFEMILGP 389
                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                        Application US/08918723
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                                 E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.O.
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77.8%;
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Pred. No.
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

COUNTRY: USA ZIP: 94304

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Patent No. 5952181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-237-507-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US, FILING DATE: Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               STREET: 31. CITY: Palo Alto
                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                       CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REGRENCE/DOCKET NUMBER: PRELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER: IBM Con
OPERATING SYSTEM:
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OPERATING SYSTEM:
                                                                                                       APPLICATION NUMBER:
                                                                                                                                                        FILING DATE:
                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                     LICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
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                              PF-0368 US
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Pred. No. 28
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Watches 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4,
                                                                                                              TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                              SEQUENCE CHARACTERISTICS LENGTH: 36 amino acid
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MOLECULE TYPE:
FRAGMENT TYPE:
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ADDRESSEE: Birch, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Matsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIAL GELLIBRARY: GELLIBRARY: 992704
                            LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                 TELEPHONE: 703-241-2848
                                                                                                                                                                                               NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30330 REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 301 N. Washington St. CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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TOPOLOGY: lir
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Suzuki, Koji
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peptide
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Pred. No. 28;
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NAME/KEY: Peptide LOCATION: 1..36 OTHER INFORMATION: /label= peptide

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; OTHER INFORMATION: /note= "Peptide III; preferred peptide to be OTHER INFORMATION: attached to C-terminus of thrombin binding; OTHER INFORMATION: polypeptide, Peptide I."

US-08-261-206A-4

Query Match
Best Local Similarity 75.0%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Search completed: March 22, 2004, 07:03:55

Job time: 1.9672 secs
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        40.5
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1 DAFEPHGYLLTAAVSPGK 18
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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hypothetical prote hypothetical prote hypothetical protein - hu alpha-2-macroglobu hypothetical prote hypothetical prote
                                                                                                                            céll division prot hypothetical precursor gastrin precursor photosynthetic reasugar transport sy hypothetical prote sigk-creating site hypothetical prote reaction center probable phloem-sp NADH-dependent fla NADH:flavin oxidor quinolone resistan chitinase (EC 3.2.
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725	716	716	716	716	545	525	471	459	451	451	262	253	251	227	209
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prot	RNA-directed RNA p	RNA-directed RNA p	RNA-directed RNA p	RNA-directed RNA p	hypothetical prote	chitinase (EC 3.2.	probable RNA bindi	probable methyltra	hypothetical prote	conserved hypothet	hypothetical prote	chlorophyll a/b-bi	hypothetical prote	hypothetical prote	glutathione S-tran

# ALIGNMENTS

Query Match 47.4%; Score 45.5; DB 2; Length 258; Best Local Similarity 55.6%; Pred. No. 6.7; Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;	e_revision 17-Sep. II, G.; Bloch, C.; ao, Y. sequence of Esche MUID:97426617; PM. ic acid sequence I ic acid sequence I N. GB:U00096; N. n. K-12, substrain othetical protein	QY 2 AFEPHGYLLTAAVSDGK 18   :  :  :      Db 393 AFKDRGWLLSAAVSDSK 409  RESULT 2 G65054 hypothetical protein b2739 - Escherichia coli (strain K-12)	de degradation 2; Length 1635 4; 2; Indels	R;de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W. Insect Mol. Biol. 7, 233-239, 1997  A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila. A;Reference number: Z17872  A;Accession: T14075  A;Status: preliminary; translated from GB/EMBL/DDBJ  A;Molecule type: DNA  A;Residues: 1-1635 <del>  A;Cross-references: EMBL;AF026492; NID:q2564720; PID:q2564721; PIDN:AAB81850.1</del>	RESULT 1  T14075  Chitthase (BC 3.2.1.14) - yellow fever mosquito  C;Species: Aedes aegypti (yellow fever mosquito)  C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999  C;Accession: T14075

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A; NEGLUE: FLYPE: DNA
A; Molecule type: DNA
A; Residues: 1-395 < XIA>
A; Residues: 1-395 < XIA>
A; Cross-references: EMBL. AL035065; PIDN: CAA22626.1;
A; Cross-references: strain 972h-; cosmid c23G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T39956
R;Xiang, Z.; Aves, S.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, January 1999
A;Reference number: Z21893
A;Accession: T39956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable nadh-dependent flavin oxidoreductase - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
hypothetical protein APE0428 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: F72736
C;Accession: F72736
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-605 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein MTH381 - Methanobacterium thermoautotrophicum (strain C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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C;Superfamily: NADPH dehydrogenase chain OYE2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MUID:98037514; PMID:9371463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan: i, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. Bacteriol. 179, 7135-7155, 1997
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Best Local
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8; Conserv
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63.6%;
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Pred. No. 29;
2; Mismatches
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Pred. No. 18;
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R.; Jiwani, N
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    A;Reference number:
A;Accession: A69733
A;Status: prelimina
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    ;Status: preliminary; nucleic acid sequence not shown;
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A;Cross-references: EMBL:AL021813; PIDN:CAA16991.1; A;Experimental source: strain 972h-; cosmid c23A1 C;Genetics:
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A;Gene: APE0428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon,
A:Reference number: A72450; MUID:99310339; PMID:10382966
A69733
PBSX prophage ORF xkdR -
PBSX prophage ORF xkdR -
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A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T38236
                                                                                                                                                                                                                                                                                                                                                                                                 R;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38236
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50.0%;
                    Bacillus subtilis
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Pred. No.
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Pred. No.
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2; Mismatches
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C;Accession: A69733
C;Accession: A6973
A;Authors: Brouillet, S.; Bruschi, C.V; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Fosh, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Fitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
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translation

not

shown

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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Reddarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolopus solfataricus complete genome.
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A,Residues: 1-88 <KUN>
A,Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13128.1; PID:e1183291
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A; Residues: 1-425 < KI
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A; Accession: H90415
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                                                                                                                                                                                                                                                                                                                                                             hypothetical protein glnA-2 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
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A;Cross-references: GB:AE001779; GB:AE000512; NID:g4981777;
A;Experimental source: strain MSB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical
                                                                                                                       Gene: glnA-2
                                                                                                                                                     Cross-references: GB:AE006641; NID:g13815744; PIDN:AAK42583.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Thermotoga maritima
;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
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Best Local :
                                                                                     Query Match
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                                                     Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi. M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                         1-425 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                   H90415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 9; Conserv
 AFEPHGYLLTAAVSP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHGYLLTAAVSPGK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAGYALTRYVFPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maltose transport protein
                                                       Conservative
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53.3%;
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Pred. No.
                                                                     Score 43; DB
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
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                                                       Mismatches
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gastrin precursor [validated] - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 31-Dec-1991 #sequence revision 23-Mar-1995 C;Accession: S14400; A4409; B01619; A01619 R;Kim, S.J.; Uhm, K.N.; Kang, Y.K.; Yoo, O.J. DNA Seq. 1, 181-187, 1991
                                                                                                       GMBO
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                                                                                                                       RESULT 12
                                                                                                                                                                                                                                             Matches
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Best Local
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349

AIKPHGYPLYSAAVS

363 15

#text\_change

20-Oct-2000

N 10;

AFEPHGY-LLTAAVS Conservative

44.3%;

2

Score 42.5; I Pred. No. 38; 2; Mismatches

DB B

<u>ب</u> *ب* 

Length 452;

Indels

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Gaps

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A;Map position: 2
A;Introns: 75/3; 171/3; 273/1; 331/3; 378/3
C;Superfamily: mammalian acid phosphatase
                                                                                                                                                                                             submitted to the EMBL Data Library,
A;Reference number: Z19292
A;Accession: T20556
                                                                                                                                                                                                                                                                                   hypothetical protein F07H5.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                      RESULT 11
T20556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell division protein FtsH - Deinococcus radiodurans (strain R1)
(;Species: Deinococcus radiodurans
(;Species: Deinococcus radiodurans
(;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
(;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
(;Accession: G75582
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D.
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
G75582
                                                           A; Gene: CESP: F07H5.9
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C;Superfamily: cell division protein ftsH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE001863;
A:Frnerimental source: strain R1
                                                                                                                                                                          A; Status: preliminary;
                                                                                                                                                                                                                                                       R;Steward,
                                                                                                                                                                                                                                                                           C; Accession: T20556
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A; Residues: 1-655 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.; Smith, H.O.; Venter, J.C.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: DRA0290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of the radioresistant bacterium Deinococcus
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: G75582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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                                                                                                                                                                            translated
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56.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
                                                                                                                                                                                                                                       December 1995
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46;
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T.; Zalewski,
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A;Residues: 1-255 <NAG>
A;Cross-references: EMB
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R;Negashima, K.V; Hiraishi, A.; Shimada, K.; Matsuura, K.

g. Mol. Evol. 45, 131-136, 1997

A;Title: Horizontal transfer of genes coding for the photosynthetic reaction centers of A;Reference number: Z17174; MUID:97383243; PMID:9236272

A;Accession: T10820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Cloning and sequencing of the bovine gastrin gene A;Reference number: A41409; MUID:90114160; PMID:2608050 A;Accession: A41409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 76-92 < AGA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 219, 614-615, 1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-3,'1',33-36,'R',38-47,'T',49-73,'N',75-80,'G',82-95,'M',97-98,'G',100-10,
A; Cress-references: GB:M31657; NID:g163079; PIDN:AAA30537.1; PID:g163080
A; Note: the authors translated the codon CTG for residue 32 as Ala, AAT for residue 39 a
R; Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Bovine and feline gastrin cDNA sequences and the amino acid and A;Reference number: S14400; MUID:92127058; PMID:1773057
                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     );Superfamily: gastrin
);Reywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic
);Reywords: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic
);1-19/Domain: signal sequence #status predicted <BGN>
);1-19/Domain: signal sequence #status predicted <BGN>
);76-92/Product: big gastrin #status experimental <SGN>
);76-92/Product: gastrin #status experimental <SGN>
);59/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
);87/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
);92/Modified site: amidated carboxyl end (Phe) (amide in mature form from followin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:X16581; NID:g648; PIDN:CAA34598.1; Lund, T.; Olsen, J.; Rehfeld, J.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                              Superfamily: reaction center protein Keywords: photosynthesis; transmembrane protein
                                                                                                                                                                                                                                 Gene:
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                                                                                         Matches
                                                                                                                                Query Match
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166
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AFGMHGSIILSVLNPGK
                                         AFEPHGYLLTAAVSPGK 18
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                                                                                       Conservative
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                                                                                                          43.8%;
182
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Pred. No. 9.9;
5; Mismatches
                                                                                                             Score 42;
Pred. No.
                                                                                       Mismatches
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25;
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RESULT 14

Search completed: March Job time : 2.17065 secs

22, 2004, 07:01:24

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A; Experimental | C; Genetics:
A; Gene: BH3690
                                                                                                                                                                                          A;BLatus, F---
A;Molecule type: DNA
A;Residues: 1-449 <WIL>
A;Residues: 1-449 <WIL>
A;Cross-references: EMBL:Z69662; PIDN:CAA93502.1; GSPDB:GN00022; CESP:F56D5.3
A;Cross-references: clone F56D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 200.
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B84111
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                                S
                                                                                                                                             A;Gene: CESP:F56D5.3
A;Map position: 4
A;Introns: 82/3; 311/3;
                                                                                                                                                                                                                                                                                                           A; Accession: T22777
                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F56D5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22777
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T22777
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: B84111
                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A;Reference number: Z19614
                                                                                                                                                                                                                                                                                                                                                                   R;Matthews,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07409.1; GSPDB:GN00:
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-420 <STO>
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 196
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8; Conservative
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206
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72.7%;
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Pred. No. 46;
0; Mismatches
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Pred. No.
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96
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q913b3
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brugia mala	lactobacill	mus musculu	homo sapien	bacillus an	saccharomyc	chlamydomon	ovis aries	lactococcus	mus musculu	chlorella v	thermotoga

### ALIGNMENTS

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RESULT 1
CHI1_DROME
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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heterochromatic sequences in a Drosophila whole-genome shotgun assembly.";
Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley;
MEDLINE=22426071; PubMed=12537574;
Moskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Sutton G.G.,
Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,
Karpen G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
EMBL; AF026500; AAB81858.1; -.
FlyBase; FBgn0022703; Cht1.
FlyBase; FBgn0022703; Cht1.
InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001279; Glyco hydro 18.
Ffam; PF00704; Glyco hydro 18; 2.
FroDom; PD000471; Glyco hydro_18; 2.
SMART; SM00636; Glyco 18; 1.
FROSTIB; PS01095; CHTTINASE 18; 1.
Hydrolase; Glycosidase; Chitin degradation; Multigene family.
ACT_SITE 264 264 PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                             Insect Mol. Biol. 7:233-239(1998).
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
acetyl-D-glucosamine polymers of chitin.
-!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
hydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE=98324849; PubMed=9662472; de la Vega H., Specht C.A., Liu Y., "Chitinases are a multi-gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 151-263 FROM N.A. STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robbins P. in Aedes,
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s, Anopheles
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                       EMBL; AF026502; AAB81860.1; -.

R FlyBase; FBgn0022701; Cht3.

R InterPro; IPR001257; Chitin_bind_PerA.

R InterPro; IPR001257; Glyco_hydro_18.

R InterPro; IPR001579; Glyco_hydro_18AS.

R InterPro; IPR001579; Glyco_hydro_18AS.

R Pfam; PF01607; CBM_14; 2.

R Pfam; PF0070471; Glyco_hydro_18; 1.

R ProDom; PD000471; Glyco_hydro_18; 1.

R ProDom; PD000471; Glyco_hydro_18; 1.

R PROSITE; SM00639; ChtBD2; 2.

R SMART; SM00636; Glyco_18; 1.

R PROSITE; PS01095; CHITINASE_18; FALSE_NEG.

R PROSITE; PS01095; CHITINASE_18; FALSE_NEG.

M Hydrolase; Glycosidase; Chitin degradation; Chitin-binding;

M Miltigene family: Parear
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Best Local
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                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             de la Vega H., Specht C.A., Liu Y., Robbins P.W.;
"Chitinases are a multi-gene family in Aedes, Anopheles and Drosophila.";
Insect Mol. Biol. 7:233-239(1998).
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages acetyl-D-glucosamine polymers of chitin.
-!- SIMILARITY: Belongs to chitinase class II (family 18 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98324849; PubMed=9662472; de la Vega H., Specht C.A., Liu Y., "Chitinases are a multi-gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426071; PubMed=12537574;
Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern
Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton
Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin
Karpen G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DROME
 Hydrolase; Glycosidase; Multigene family; Repeat DOMAIN 5 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Canton-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 182-294 FROM N.A.
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Ephydroidea; Drosophilidae; Drosophila
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Eukaryota; Metazoa; Arthropoda; Hexa
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                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 2 chitin-binding type-2 domains.
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11; Conserv
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   Repeat.
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64.7%;
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Pred. No.
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a; Brachycera; Muscomorpha;
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Ecodene; EG13107; ygbM.
Ecodene; EG13107; ygbM.
InterPro; IPR001719; AP_endnuclease2.
Pfam; pF01261; AP_endonuc_2; 1.
Pfam; pF01261; AP_endonuc_2; 1.
Hymothetical protein; Complete proteome; 3D-structure.
Hymothetical protein; Complete proteome; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blattner F.R., Piunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q46891;
01-NOV-1997
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YGBM OR B2739
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10-OCT-2003
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Enterobacteriaceae; Escherichia.
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H.INFLUENZAE HI1013.
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1K77; 30-OCT-02
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Pred. No. 0.66
4; Mismatches
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4A063190B7E96248 CRC64;
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Pred. No. 4.
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Pfam; PF00136; DNA pol B; 2.
Pfam; PF03104; DNA pol B exo; 1.
Pfam; PF03104; DNA pol B exo; 1.
SMART; SM00305; HintC; 2.
SMART; SM00306; HintN; 2.
SMART; SM00306; HintN; 2.
SMART; SM00486; POLBC; 1.
TIGRPAMS; TIGR01443; intein Cterm; 2.
TIGRPAMS; TIGR01443; intein Nterm; 2.
TIGRPAMS; TIGR01445; intein Nterm; 2.
TIGRPAMS; TIGR00592; pol2; 1.
PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                        InterPro; IPR006172; DNA pol B.
InterPro; IPR006134; DNA pol B dom.
InterPro; IPR006134; DNA pol B exo.
InterPro; IPR006133; DNA pol B exo.
InterPro; IPR003587; Hedgehog hint N.
InterPro; IPR003586; Hedgehog hint C.
InterPro; IPR006142; INTEIN.
InterPro; IPR006141; Intein endonuc.
InterPro; IPR006141; Intein S.
InterPro; IPR006141; Intein S.
InterPro; IPR0061478; Pol 2.
InterPro; IPR0061478; Pol 2.
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Saves I., Ozanne V., Dietrich J., Masson J.-M.;
With distinct enzymatic behaviors.";
With distinct enzymatic behaviors.";
J. Biol. Chem. 275:2335-2341(2000).
J. Biol. Chem. 275:2335-2341(2000).
J. FUNCTION: PI.-True recognizes and cleaves a minimal sequence of 1
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modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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HSSP; P56689; 1TGO.
REBASE; 4500; PI-TfuI.
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Submitted (FEB-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTW: This protein undergoes a protein self splicing that a post-translational excision of the two intervening regi (inteins) followed by peptide ligation.

SIMILARITY: Belongs to the DNA polymerase type-B family.

SIMILARITY: In the intein section; belongs to the homing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              base pairs (bp) on supercoiled DNA with either Mn(2+) or Mg(2+) a cofactor. It cleaves linear DNA only with Mn(2+) and requires a 19-bp minimal recognition sequence. The optimal temperature for activity is 70 degrees Celsius.

FUNCTION: PI-TfuII is a highly active homing endonuclease using Mg(2+) as cofactor. Its minimal recognition and cleavage site is 21 bp long either on linear or circular DNA substrates. Its endonuclease activity is strongly inhibited by the 3' digestion product, which remains bound to the enzyme after the cleavage reaction. The optimal temperature for activity is 70 degrees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endonuclease family.
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pol-1 intein);
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PROSITE; PS50819; INTEIN_TER; 2.

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W Transferase; DNA-directed DNA polymerase; DNA replication; Manghasium; M
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                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella aerogenes.
Bacteria; Proteobacteria;
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DR Pfam; PF03136; DNA_Dol B; 3.
DR Pfam; PF0314; DNA_Dol B; 3.
DR Pfam; PF0314; DNA_Dol B_exo; 1.
DR Pfam; PF03194; DNA_Dol B_exo; 1.
DR PRINTS; PR00379; INTEIN.
DR SMART; SM00305; HintC; 2.
UR SMART; SM00305; HintC; 2.
R SMART; SM00486; POLBC; 1.
R TIGRPAMS; TIGR01443; Intein_Cterm; 2.
TIGRPAMS; TIGR01445; Intein_Nterm; 2.
TIGRPAMS; TIGR0145; Intein_Nterm; 2.
PROSITE; PS00116; DNA_DOLYMERASE B; FALS; PROSITE; PS50818; INTEIN_ENDONUCLASE; 2.
PROSITE; PS50819; INTEIN_NTER; 2.
Transferase; DNA_divertal_LER; 2.
Transferase; DNA_divertal_
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InterPro; IPR006133; DNA_pol_B_exo.
InterPro; IPR003587; Hedgehog_hint_N.
InterPro; IPR003586; Hedgehog_hint_C.
InterPro; IPR003586; Hedgehog_hint_C.
InterPro; IPR006142; Intein_endonuc.
InterPro; IPR006142; Intein_endonuc.
InterPro; IPR006141; Intein_S.
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Saves I., Eleaume H., Dietrich J., Masson J.-M.;
Saves I., Eleaume H., Dietrich J., Masson J.-M.;
"The Thy pol-2 intein of Thermococcus hydrothermalis is an
isoschizomer of PI-TliI and PI-TfuII endonucleases.";
Nucleic Acids Res. 28:4391-4396(2000).
Nucleic Acids Res. 28:4391-4396(2000).
-I-FUNCTION: In addition to polymerase activity, this DNA polymerase
exhibits 3' to 5' exonuclease activity (By similarity).
-I-FUNCTION: PI-THYI AND PI-THYII ARE ENDONUCLEASES. PI-THYI CLEAVES
-I-FUNCTION: PI-THYI AND PI-THYII ARE ENDONUCLEASES. PI-THYI CLEAVES
-I-FUNCTION: PI-THYI AND PI-THYI DNA POL GENE. IT REQUIRES A 21-
BP MINIMAL RECOGNITION SEQUENCE.
-I- CATALLYTIC ACTIVITY: N deoxymucleoside triphosphate = N diphosphate
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SEQUENCE FROM N.A., Lesongeur F.O., Barbier G.;

"Thermococcales taxonomy and phylogeny based on the comparative use (
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REBASE; 4832; PI-ThyI.
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                                                                         DNA-binding;
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SIMILARITY: Belongs to the DNA polymerase type-B family.

SIMILARITY: In the intein section; belongs to the homing
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Guiseppi G., Guy B.J., Haga K., Haisech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haisech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
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RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Noone D., O'Railly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Pareo U., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rappoort G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Schight J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Schight J., Tanakshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Yoshida K., Yoshikawa H.F., Zumste K., Yasmoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumste I., Yasmoto K., Yata K.,
Ra Yoshida K., Yatamoto H., Waller B., Yata K.,
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01-0CT-1996 (Rel. 34, Created)
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Phage-like element PBSX protein xkdR.
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Bacteria; Firmicutes;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                            Subtilis.;
Nature 390:249-256(1997).
Nature 370:249-256(1997).
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P01352; Q28114;
21-JUL-1986 (Rel
01-NOV-1991 (Rel
28-FEB-2003 (Rel
                                                                                                                                                                                                                                                        Agarwal K
Sheppard
                                                                                                                                                                                                                                                                                                                             MEDLINE=92127058; PubMed=1773057; Kim S.J., Uhm K.N., Kang Y.K., Yoo O.J.; "Bovine and feline gastrin cDNA sequences and the amino acid and nucleotide sequence homologies among mammalian species."; DNA Seq. 1:181-187(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                          This
                                                                                                                                                                                                              Agarwal K.L., Beacham J., Bentley P.H., Gregory R Sheppard R.C., Tracy H.J., "Isolation, structure and synthesis of ovine and Nature 219:614-615(1968).

-!- FUNCTION: Gastrin stimulates the stomach muco
                                                                                                                                                                                                                                                                        MEDLINE=68357500; PubMed=5665711; Agarwal K.L., Beacham J., Bentley
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Lund T., Olsen J., Rehfeld J.F.;
"Cloning and sequencing of the bovine gastrin gene.";
Mol. Endocrinol. 3:1585-1588(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90114160; PubMed=2608050;
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Bovidae; Bovinae; Bos
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                                                  modified and this statement
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                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
                                        entities requires a
                                                                                              between
                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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; Z99110; CAB13128.1;
A69733; A69733.
                                                                                                                                                              and increases blood circulation and water and intestine.
                                                                                                                                                                                         secrete hydrochloric acid and the pancreas to secrete its digestive enzymes. It also stimulates smooth muscle contra
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                          an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                         Gregory R.A.,
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RESULT 9
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Best Local &
Matches
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                                                                                                                                                                                                                                                                                                                                                                                   Nagashima K.V., Hiraishi A., Shimada K., Matsuura K.;
Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
-I-FUNCTION: THE REACTION CENTER IS A MEMBRANE-BOUND COMPLEX THAT
MEDIATES THE INITIAL PHOTOCHEMICAL EVENT IN THE ELECTRON TRANSFER
PROCESS OF PHOTOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Hormone; Cleavage on pair of basic residues; Amidation; Signal; Phosphorylation; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00918; Gastrin; 1
SMART; SM00029; GASTRIN;
                   EMBL;
                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodospirillum photometricum.
Bacteria; Proteobacteria; Alphaproteobacteria;
Rhodospirillaceae; Rhodospirillum.
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751750;
71-0CT-1996 (Rel. 34, Createq;
71-0CT-1996 (Rel. 34, Last sequence update)
710-0CT-2003 (Rel. 42, Last annotation update)
72-7203 (Rel. 42, Last annotation update)
73-7205 (Rel. 42, Last annotation update)
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PIR; S14400;
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                                                                                                                                                                                                                                                                                                 SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIO TWO DACTERIOPHEOPHYTINS, TWO UBIQUINONES, ONE IRON, HIGHLY HYDROPHOBIC POLYPEPTIDE CHAINS (DESIGNATED L, SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
PSBD FAMILY.
                   D50681; BAA09329.1; ~. P06009; 6PRC.
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                                                                                                                                                                                                                                                                           Integral membrane protein.
THE REACTION CENTER L/M CHAINS / PSBA /
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A -> L (IN REF. 1).

G -> R (IN REF. 1).

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AMIDATION (G-93 PRO
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(BY SIMILARITY).
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E IRON, AND THREE
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RESULT 10
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TIGRFAMS; TIGR0115
PROSITE; PS00244;
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HAMAP; MF_00653; -; 1.
PQQ biosynthesis; Transport.
SEQUENCE 304 AA; 32323 MW;
                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria; Alphaproteobacteria; R
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                                                              EMBL; AJ277117; CAB83198.1;
                                                                                                                     entities
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                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                               PATHWAY: Pyrrologuinoline quinone (PQQ) biosynthesis. SIMILARITY: Belongs to the pqqB family.
                                                                                                                                                                                                                                                                                        Microbiol. Lett. 193:231-236(2000).
FUNCTION: May be involved in the transport of
to the periplasm (By similarity).
PATHWAY: Pyrrologninoline quinone (PQQ) biosym
                                                                                                                                                                                                                                                                                                                                                                                      pyrroloquinoline
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PS00244; REACTION_CENTER; 1.
transport; Photosynthesis; Reaction center;
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                                                                                                                                                                                                                                                                                                                                                                                      Gupta A., Verma V., Kumar A., Qazi
loquinoline quinone synthesis genes
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 42, Last annotation update)
Q synthesis protein B (Pyrroloquinoline sprotein B).
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LIGAND) (BY SIMI)
IRON (NON HEME)
IRON (NON HEME)
QUINONE B (BY SI)
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Pred. No.
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LIGAND) (BY SIMILARITY).
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  E9C54F778A8E2732 CRC64;
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E Gluconobacter
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Query Match

43.8%;

Score 42;

DB 1; Length 304;

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RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cammings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cammings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cammings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Connerton I.F., Cammings N.J., Daniel R.A.,
RA Chispit G., Galizri A., Galizzi A., Galieron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galieron N.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Purnelle B., Rosetl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sendaie Y.,
RA Sekiguchi J., Sechus A., Serorr S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
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01-AUG-1990
01-AUG-1990
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STRALN=168 / JH642;
MEDLINE=55219086; PubMed=7704261;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
"Complete nucleotide sequence of a skin element excised by DNA rearrangement during sporulation in Bacillus subtilis.";
Microbiology 141:323-327(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=90130265; PubMed=2105293;
Sato T., Samori Y., Kobayashi Y.;
The cisA cistron of Bacillus subtilis sporulation gene spoIVC
encodes a protein homologous to a site-specific recombinase.";
J. Bacteriol. 172:1092-1098(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative DNA recombinase. CISA OR SPOIVCA OR BSU25770.
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Kobayashi Y.;
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MEDLINE=97124195; Po
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Bacteria; Firmicutes; Bacillales;
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PubMed=8969508;
Takemaru K.-I.,
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RESULT 12
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01-JUL-1989
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A99117; CAB1*-
A43656; A43656.

111st; BG10458; cisA.
2017PO; IPR006118; Recombinase.
cerPro; IPR006119; resolvase_N.
2017E; P800399; RECOMBINASES_1; 1.
2017E; P800399; RECOMBINASES_2; FALSE_NEG.
PROSITE; P800398; RECOMBINASES_2; FALSE_NEG.
PROSITE; P800399; RECOMBINASES_10A-binding; Complete protecombination; DNA integration; DNA-binding; Complete protecombination; DNA integration; DNA-CEAVAGE TO DNA STRAND CLEAVAGE AND REJOINING
(BY SIMILARITY).

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Viari A., Wambutt R., Wedler E., Wedler H., Weitzen
Winters P., Wipat A., Yamamoto H., Yamane K., Yasum
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa
"The complete genome sequence of the Gram-positive
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EMBL; D32216; BAA06971.1; -.
EMBL; D84432; BAA12435.1; -.
EMBL; Z99117; CAB14518.1; -.
MEDLINE=84133817; PubMed=6199280;
MEDLINE=84133817; PubMed=6199280;
Theiler R., Suter F., Zuber H.;
"N-terminal sequences of subunits
                                                                                                              Belanger G., Berard J., Corriveau P., 
"The structural genes coding for the 
Rhodospirillum rubrum photoreaction c 
J. Biol. Chem. 263:7632-7638(1988).
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                                                                                                                                                                                                                                                                                                                                                                                         subunit).
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shikawa H., Danchin A.;
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ACCOMENS ACCORDANT ACCOR

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Alphaherpesvirinae; NCBI\_TaxID=10310;

Simplexvirus.

SEQUENCE

FROM

N.A

Herpes simplex virus (type Viruses, no

pe 2). no RNA stage; Herpesviridae;

P06489; Q69352; 01-JAN-1988 (Rel. 06, Created) 01-JAN-1988 (Rel. 06, Last sequence up 15-JUL-1998 (Rel. 36, Last annotation Alkaline exonuclease (EC 3.1.11.-).

update)

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HSV2

STANDARD;

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RESULT 13
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SEQUENCE
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hoppe-Seyler's Z. Physiol. Chem. 364:1765-1776(1983).
-i- FUNCTION: THE REACTION CENTER IS A MEMBRANE-BOUND COMPLEX THAT MEDIATES THE INITIAL PHOTOCHEMICAL EVENT IN THE ELECTRON TRANSFER PROCESS OF PHOTOSYNTHESIS.
                                                                                                                                                                                                 METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reaction centre from Rhodos
subunits by gel filtration
organic solvents.";
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TIGKPAMs; TIGR01157; puTL; 1.
PROSITE; PS00244; REACTION CENTER; 1.
Electron transport; Photosynthesis; Reaction center;
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                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                      Bacteriochlorophyll;
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PRINTS; PR00256; REACTNCENTRE.
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005871; Photo_RC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOCHLOROPH TWO BACTERIOPHEOPHYTINS, TWO UBLQUINONES, ONE IRON, AND THESE HIGHLY HYDROPHOBIC POLYPEPTIDE CHAINS (DESIGNATED L, M, AND H SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA PSBD FAMILY.
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                                                                                    HGYLLTAAVSPGK 18
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                                                                                                                        42.7%;
53.8%;
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                                                                                                                                                                                                                                                                                                                                      Magnesium;
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IRON (N
                                                                                                                        Score 41;
Pred. No.
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                                                                                                                                                                                     IRON
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                                                                                                                                    Length 275;
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Sephadex G 100 in
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Query Match
Best Local S
Matches 7
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Q9NYQ7; O75092;
28-FEB-2003 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86144016; PubMed=3005609;
Draper K.G., Devi-Rao G., Costa R.H., Blair E.D., Thompson R.L.,
Wagner E.K.;
"Characterization of the genes encoding herpes simplex virus type
"Characterization exonucleases and overlapping proteins.";
J. Virol. 57:1023-1036(1986).
                                                                                                                 Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., I'dentification of high-molecular-weight proteins with mu EGF-like motifs by motif-trap screening.", Genomics 51:27-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Cadherin EGF LAG seven-pass G-type receptor 3
homolog 1) (hFmil) (Multiple epidermal growth
(Epidermal growth factor like 1).
CELSR3 OR CDHF11 OR FMII OR EGFL1 OR MEGF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M11854; AAA45834.1; ---
EMBL; M11854; AAA45835.1; ALT INIT.
EMBL; M11854; AAA45835.1; ALT INIT.
InterPro; IPR001616; Herpes_alk_exo; 1.
PRINTS; PR01771; Herpes_alk_exo; 1.
PRINTS; PR00924; ALKEXNUCLASE.
Hydrolase; Nuclease; Exonuclease; 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                         SEQUENCE OF 1954-3312 FROM N.A.
                                                                                                                                                                                                                                                                   feature
                                                                                                                                                                                                                                                                       "Large exons encoding multiple ectodomains are a characteristic
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=20202599; PubMed=10716726;
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                          MEDLINE=98360089; PubMed=9693030;
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signaling during nervous system formation.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 2 of G-protein cou
SIMILARITY: Contains 9 cadherin domains.
SIMILARITY: Contains 8 EGF-like domains.
SIMILARITY: Contains 1 laminin G-like domains.
SIMILARITY: Contains 1 laminin EGF-like domains.
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. Acad. Sci. U.S.A.
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Pred. No.
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factor-like
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Pfam; PF00028; cadherin; 9
Pfam; PF00008; EGF; 5.
Pfam; PF01825; GPS; 1.
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EMBL; AB011536;
HSSP; P00740; 1E
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EGF-like d
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PROSITE;
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                     AAF61929.1; -.
BAA32464.1;
                                                                                                    (See http://www.isb-sib.ch/announce/
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GO; GO:0005198; F:structural molecule activity; NAS. InterPro; IPR000152; Asx hydroxyl\_S. InterPro; IPR002126; Cadherin. InterPro; IPR002126; ConA like\_lec\_gl. InterPro; IPR001885; ConA like\_lec\_gl. InterPro; IPR001881; EGF\_Z. InterPro; IPR001881; EGF\_Ca. InterPro; IPR001881; EGF\_Ca. InterPro; IPR001882; GPCR secretin. InterPro; IPR001879; horm\_receptor. InterPro; IPR001791; InterPro; IPR000203; Laminin\_G.
PKD\_cys\_rich. hormn\_receptor. Laminin\_EGF.

Pfam; PF02793; HRM; 1.
Pfam; PF00054; laminin G; 2.
PRINTS; PR00205; CADHERIN.
PRINTS; PR00211; EGFLAWININ
PRINTS; PR00249; GPCRSECRETI
SMART; SM00112; CA; 9.
SMART; SM00181; EGF; 6.
SMART; SM00303; GPS; 1.
SMART; SM00008; HormR; 1. SM00282; LamG; GPCRSECRETIN. EGFLAMININ 9 Ν.

FALSE\_NEG.

; SMOOJ82; LamG; 2.
; SMOOJ82; LamG; 2.
; SMOOJ82; LamG; 2.
; SMOOJ82; CADHERIN 1; 7.
FE; PSOOJ32; CADHERIN 2; 8.
FE; PSOOJ32; CADHERIN 2; 8.
FE; PSOOJ22; EGF 1; 6.
FE; PSOOJ22; EGF 2; 4.
FE; PSOOJ22; EGF 3; 6.
FE; PSOOJ24; EGF 3; 6.
FE; PSOOJ24; GPROTEIN RECEP F2 1; FALSE NIFE; PSOOJ27; GPROTEIN RECEP F2 3; 1.
FE; PSOJ27; GPROTEIN RECEP F2 4; 1.
FE; PSOJ27; GPROTEIN RECEP F2 4; 1.
FE; PSOJ27; GPROTEIN RECEP F2 4; 1.
FE; PSOJ27; GPROTEIN TYPE EGF; 1.
FE; PSOJ248; LAMININ TYPE EGF; 1.
FE; PSOJ248; LAMININ TYPE EGF; 1.
FE; PSOJ248; LAMININ TYPE EGF; 1.
FI; PSOJ248; LAMI : Glycoprotein; EGF-like domai domain; Repeat;

2541 25562 2573 2594 2602 26623 26623 26644 26623 2703 2703 2703 2747 3312 2540 2561 2572 2593 2601 2662 26643 26643 26643 2702 27725 27725 1 (POTENTIAL).
CYTOPLASMIC (P
2 (POTENTIAL).
EXTRACELLULAR
3 (POTENTIAL).
CYTOPLASMIC (P CYTOPLASMIC (F 6 (POTENTIAL). EXTRACELLULAR EXTRACELLULAR 5 (POTENTIAL) RECEPTOR 3. EXTRACELLULAR CADHERIN EGF LAG RECEPTOR 3. POTENTIAL (POTENTIAL) (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL) SEVEN-PASS G-TYPE

TRANSMEM
DOMAIN

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DAWDPHTHVLLPSQSP
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CADHERIN 3.
CADHERIN 5.
CADHERIN 6.
CADHERIN 6.
CADHERIN 7.
CADHERIN 9.
EGF-LIKE 1, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
EGF-LIKE 4, CALCIUM-BINDING.
EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
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CYTOPLASMIC (F
CADHERIN 1.
CADHERIN 2.
                                                                                                                                                                          Score 41; DB
Pred. No. 3.1e
5; Mismatches
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                                                                                                                                                                                                                                          Length 3312;
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CRC64;
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RESULT 15
CLR3 RAT
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ID CLR3 RAT
AC 088278;
DT 28-FEB-2003 |
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DT 10-CCT-2003 |
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JEPTO, IPRO06210;

LITERYPO, IPRO02049; L.

INTERPRO01791; Lan

INTERPRO01791; Lan

Pfam; PF00002; Tum 2; 1.

Pfam; PF000028; GGP; 1.

Pfam; PF000038; GGP; 1.

Pfam; PF001825; GPS; 1.

Pfam; PF001825; GPS; 1.

Pfam; PF001825; GPS; 1.

Pfam; PF001825; GADHERIN.

"NTS; PR00205; CADHERIN.

"NTS; PR00205; CADHERIN.

"TS; PR00205; CADHERIN.

"SW00111; EGF; 6.

"W00303; GPS; 1.

"000008; HOT"

"000008; HOT"

"189
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c -i- SUBCELLULAR LOCATION: Integral membrane protein.
c -i- TISSUE SPECIFICITY: Expressed in the brain. Expressed in cerebrellum, olfactory bulb, cerebral cortex, hippocampus and brain stem.
c -i- SIMILARITY: Belongs to family 2 of G-protein coupled receptor c -i- SIMILARITY: Contains 9 cadherin domains.
c -i- SIMILARITY: Contains 8 EGF-like domains.
c -i- SIMILARITY: Contains 1 laminin EGF-like domains.
c -i- SIMILARITY: Contains 1 laminin EGF-like domains.
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InterPro; IPR001879;
InterPro; IPR006210;
InterPro; IPR002049;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 3
epidermal growth factor-like domains 2).
CELSR3 OR MEGF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=Sprague Dawley; TISSUE=Brain;
MEDLINE=98360089; PubMed=9993030;
Nakayama M., Nakajima D., Nagase T., Nomura
"Identification of high-molecular-weight pro
EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998)
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Mammalia; Eutheria; Rodentia;
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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InterPro; IPR001881;
InterPro; IPR006209;
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P00740; 1
   ; HormR; 1.
; LamG; 2.
LO; ASX_HYDROXYL;
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ConA like lec_gl.

EGF Z.

EGF Ca.

EGF like.

GPCR secretin.

hormn receptor.

IEGF.
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Q9u6r7 dermatophag
Q8mp05 tenebrio mo
Q8ish5 araneus ven
P91773 penaeus jap
O17412 aedes aegyp
O17412 aedes aegyp
O1593 penaeus jap
Q8ms85 drosophila
Q88ih7 pseudomonas
Q8itu3 penaeus van
Q9w092 drosophila
Q9w092 drosophila
Q9w091 descherichia
Q9f8r7 escherichia
Q9f8r7 escherichia
                                                                                                                                                                  Description
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## ALIGNMENTS

% B O	O C C C C C C C C C C C C C C C C C C C	RESILT
Query Match 100.0%; Score 96; DB 5; Length 555; Best Local Similarity 100.0%; Pred. No. 2.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Q9UGR7, Q9UGR7	TT.P 1
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DAFEPHGYLLTAAVSPGK

18

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RESULT
Q81SH5
ID Q81SH5
AC Q8

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"A Novel putative insect Chitinase with multiple catalytic dom try in hormonal regulation during metamorphosis.";

It submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ487081; CAD31740.4;

R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0008861; F:chitin binding; IEA.

R GO; GO:0008843; F:endochitinase activity; IEA.

R GO; GO:0008843; F:endochitinase activity; acting on glycosyl bonds; GO:00006520; P:amino acid metabolism; IEA.

R GO; GO:0006520; P:amino acid metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism: IFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local &
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REMBL, AJ487081; CAD31740.4;

REMBL, AJ487081; CAD31740.4;

RGO; GO:0005576; C:extracellular; IEA.

RGO; GO:0008061; F:chitin binding; IEA.

RGO; GO:0008043; F:endochitinase activity; IEA.

RGO; GO:0008632; F:hydrolase activity, acting

RGO; GO:0005575; P:carbohydrate metabolism; IEA.

RGO; GO:0005975; P:carbohydrate metabolism; IEA.

RINTERFO; IPR001223; Glyco_hydro_18A.

RINTERFO; IPR001255; Chitin bind PerA.

RINTERFO; IPR001259; Glyco_hydro_18AS.

RINTERFO; IPR00127; Glyco_hydro_18AS.

RINTERFO; IPR001579; Glyco_hydro_18AS.

RINTERFO; IPR001579; Glyco_hydro_18 S.

PFAMD; PF01607; CBM_14; 5.

PFAMD; PF01607; CBM_14; 5.

PFAMD; PF01607; CBM_14; 5.

PFAMD; PF01607; CBM_14; 5.

PRODOM; PD000471; Glyco_hydro_18; 5.

PRODOM; PD000471; Glyco_hydro_18; 5.

PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.

Signal; Hydrolase; Glycosidase.

SIGNAL

POTENTIAL.
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Q8MP05;
01-OCT-2002
                                                                                                                                                                                    01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                             Q8ISH5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Tenebrionidae; Tenebrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tenebrio molitor (Yellow mealworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitinase precursor
                                           Eukaryota; Metazoa; Arthrop
Araneomorphae; Entelegynae;
NCBI TaxID=182803;
                                                                                                                                    Araneus ventricosus.
                                                                                                                                                                 Chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7067;
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                                                                                                                                                                                                                                                                                                                                                                                                                            AFKPKGYLLSAAVSPSK 1661
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2838 AA;
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
ecursor (EC 3.2.1.14).
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                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2838
                                                                                Arthropoda; Chelicerata; Arachnida; Araneae;
legynae; Araneoidea; Araneidae; Araneus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321407 MW; 608B3F2A8E98B9B7 CRC64;
                                                                                                                                                                                       23,
25,
                                                                                                                                                                                 Created)
Last sequ
Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67; DB : Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                       sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                             431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>٠</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2838;
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RESULT 5 017412 ID 017412

PRELIMINARY;

PRT;

1635

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RESULT
P91773
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Matches
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Best Local S
Matches 12
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GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0005975; P:carbohydract metabolism; IEA.

InterPro; IPR001223; Glyco_hydro_18.

InterPro; IPR001279; Glyco_hydro_18AS.

Pfam; PF00704; Glyco_hydro_18; 1.

ProDom; PD000471; Glyco_hydro_18; 1.

PYDD0m; PM000471; Glyco_hydro_18; 1.

PROSITE; PS01095; CHITINASE_18; 1.

SEQUENCE 431 AA; 47238 MW; 929439397B9BC923 CR
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                                                                                                                                                                                                                                                                                                     GO; GO:0006030; P:chitin metabolism; IEA InterPro; IFR002557; Chitin bind perA. InterPro; IFR002557; Chitin bind perA. InterPro; IFR001579; Glyco_hydro_18. InterPro; IFR001579; Glyco_hydro_18AS. Pfam; pP01607; CBM_14; 1. Pfam; pP00704; Glyco_hydro_18; 1. ProDom; pD000471; Glyco_hydro_18; 1. SMART; SM00636; Glyco_18; 1. SMART; SM00636; Glyco_18; 1. PROSITE; PS011095; CHITINASE 18; 1. Glycosidase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D89751; BAA14014.1; --
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000861; F:chitin binding; IEA.
GO; GO:0016798; F:hydrolase activity, acting on
GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe T., Kono M.;
"Isolation of a cDNA Encoding a Chitinase Family Protein
Cuticular Tissues of the Kuruma Prawn Penaeus japonicus."
Zool. Sci. 0:0-0(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Eumalacostraca; Eucarida; Decapo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P91773;
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P91773
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penaeus japonicus (Kuruma prawn).
                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=27405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penaeidae; Marsupenaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE
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301
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                                                                   N
                                                                                                                                       12;
                                                                                                                                                                           Similarity
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                                                                   AFEPHGYLLTAAVSP 16
   AFKPHGLLLSAAVSP 315
                                                                                                                                                                                                                                                                                   527
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                                                                                                                                                                                                                                                                               AA,
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                                                                                                                                                                                                                                                                            59162 MW;
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                                                                                                                                                                       65.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
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Pred. No. 0.02;
2; Mismatches
                                                                                                                                       2
                                                                                                                                                                       Score 63;
Pred. No.
                                                                                                                                                                                                                                                                               B9CBAEAB8CDF8710 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crustacea; Malacostraca;
oda; Dendrobranchiata; Pe
                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEA.
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                                                                                                                                                                                                        DB 5;
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                                                                                                                                                                                                        Length 527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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RESULT
O15993
ID 993
AC O1
DT 01
DT 01
DT 01
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InterPro; IPR002557; Chitin bind perA.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001279; Glyco_hydro_18AS.
Pfam; PF001607; CBM_14; 3.
Pfam; PF001704; Glyco_hydro_18; 3.
ProDom; PD000471; Glyco_hydro_18; 3.
ProDom; PD000471; Glyco_hydro_18; 3.
SMART; SM00494; ChtBD2; 3.
SMART; SM00494; ChtBD2; 3.
SMART; SM00636; Glyco_Bl; 3.
PROSITE; PS01095; CHITINASE 18; 3.
PROSITE; PS01095; CHITINASE 18; 3.
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GO; GO:0005576; C:ext:
GO; GO:0008061; F:chit
GO; GO:0008843; F:endt
GO; GO:0016798; F:hydd
GO; GO:0005975; P:cax)
GO; GO:0006032; P:chit
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01-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
NCBI_TaxID=7159;
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                                                                                                                 Penaeus japonicus (Kuruma prawn).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Pe
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-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
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                                                     NCBI_TaxID=27405
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                                                                                            Penaeidae; Marsupenaeus
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GO:0008061; F:chitin binding; IEA.
GO:0008843; F:endochitinase activity; IEX
GO:0016798; F:hydrolase activity, acting
GO:0005975; P:carbohydrate metabolism; II
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Pred. No.
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InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18.
Pfam; PF01607; CBM 14; 1.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00494; ChtBD2; 1.
SMART; SM00494; ChtBD2; 1.
SMART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; 1.
SEQUENCE 467 AA; 51765 NW; 499F709577
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01-0CT-2002
01-0CT-2003
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                                                                                                           Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY119021; AAM50881.1; -
FlyBase; FBgn0063117; BcDNA:LP04696.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000561; F:chitin binding; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016030; P:chitin metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001257; Chitin bind PerA.
InterPro; IPR0012537; Chitin bind PerA.
Ffam. PB01627. CMM 14.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresenk D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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HSSP, P07254; ICTN.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:00016787; F:hydrolase activity; IEA.
GO; GO:00016795; P:carbohydrate metabolism;
GO; GO:0006030; P:chitin metabolism; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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nilarity 70.6%;
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55.6%;
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Pred. No.
   Score 53;
Pred. No.
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499F7095774CA445 CRC64;
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RESULT Q8 ITUS AC Q8 ITUS Q8 ITUS Q8 ITUS Q8 AC Q8 DF Q0 C1 DF Q0 C1 DF Q0 C2 FR Q0 C2 FR Q0 C2 FR Q0 C2 FR Q0 C3 FR Q0 C4 FR Q0 
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Best Local
                            QBITU3
QBITU3;
QBITU3
QBIT
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Complete
SEQUENCE
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Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Holmes N.
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes N.
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple B., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003313; AraC_binding.
InterPro; IPR003005; HTHARAC.
Pfam; PF02311; AraC_binding; 1.
Pfam; PF00165; HTH_AraC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003
01-OCT-2003
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GO; GO:000562;
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GO:0005622; C:intracellular; IBA.
GO:0005700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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56.2%;
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Pred. No. 7
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Mismatches
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,

Ba Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Parvier S., Dietz S.M.,

A Cherry J.M., Cawley S., Dahlke C., Parvier S., Dietz S.M.,

Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

XA Jalali M., Kalush F., Karpen G.H., Ke Z., Kanison J.A., Ketchum K.A.,

XA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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R. InterPro; IPR001252; Glyco_hydro_18AS. Ffam; PF01607; CBM 14; 1.
R. Ffam; PF01704; Glyco_hydro_18; 1.
R. Pfam; PF007047; Glyco_hydro_18; 1.
R. Probom; PD000471; Glyco_hydro_18; 1.
R. SMART; SM00639; ChtBD2; 1.
R. SMART; SM00639; Glyco_119; 1.
R. FROSTIE; PS01195; CHTTINASE_18; 1.
R. FROSTIE; PS01195; CHTTINASE_18; 1.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., Ganartides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Standet R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Champe M., Pfeiffer B.D. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.(Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., Rayendale J., Bayraktarodlu L., Beasley E.M.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Berkeley;
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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64.7%;
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sor (EC 3.2.1.14) (LD28264p).
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A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.
T "The genome sequence of Drosophila melanogaster.";
Cscience 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                     EMBL; AB003472; AAF47562.1; -.

EMBL; AV058589; AAFL13818.1; -.

EMBL; RP026501; AABB1859.1; -.

EMBL; PR026501; AABB1859.1; -.

HSSP; P07254; ICTN.

FlyBase; FBgn0022702; Cht2.

GO; GO:0008843; F:endochitinase activity; IEA.

GO; GO:0016798; F:hydrolase activity, acting on gl
GO; GO:0016798; F:carbohydrate metabolism; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0006032; P:chitin catabolism; IEA.

InterPro; IFR001579; Glyco_hydro_18.

InterPro; IFR001579; Glyco_hydro_18.

ProDom; PD000471; Glyco_hydro_18; 1.

ProDom; PD000471; Glyco_hydro_18; 1.

ProDom; PD000471; Glyco_hydro_18; 1.

SMART; SM00636; Glyco_18; 1.
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Best Local :
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Q90711
Q90711;
01-NOV-1996
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ACT SITE
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                      ProDom; PD000471; Glyco hydro 18; SMART; SM00636; Glyco 18; 1. PROSITE; PS01095; CHITINASE 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98324849; PubMed=9662472; de la Vega H., Specht C.A., Liu Y., "Chitinases are a multi-gene family
                                                                                                                                                                                                                                                                                                              Hydrolase;
Multigene
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8; Conserv
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                                                                                                                                                                                                                                                                                                              family;
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                                                                                                                                                                                                                                                                                                                       Glycosidase; Chitin degradation; Glycoprotein;
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27
168
133
 (TrEMBLrel. 01,
                                                                                                                                                              Conservative
                              PRELIMINARY;
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133
133
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   Created)
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Pred. No. 46;
4; Mismatches
                                                                                                                                                                                                                                    PROBABLE CHITINASE 2.
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTEN
N-LINKED (GLCNAC. . .) (POTEN
                                                                                                                                                                                                                                                                                               POTENTIAL.
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Best Local S
Matches
                  InterPro; IPR00163; EAL.
InterPro; IPR00318; GAF.
InterPro; IPR00318; GAF.
InterPro; IPR003160; GGDEF.
InterPro; IPR001294; Phytochrome
Pfam; PP00563; EAL; 1.
Pfam; PP00563; EAL; 1.
Pfam; PP00990; GGDEF; 1.
Pfam; PP00360; phytochrome; 1.
Pfam; PP00360; phytochrome.
PRINTS; PR01033; PMYTOCHROME.
SMART; SM000267; DUP1; 1.
SMART; SM00055; GAF; 1.
TIGRPAMS; TIGR00254; GGDEF; 1.
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O8VRN4;

O1-MAR-2002 (TIEMBLIEL 2

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NON TER
SEQUENCE
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J. Biol. Chem. 271:8895-8902(1996).
EMBL; U48890; AAC59882.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
^^^^anta anria: Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                           MEDLINE=21617697; PubMed=11742406;
Bhoo S.H., Davis S.J., Walker J., Karni
"Bacteriophytochromes are photochromic
                                                                                                                                                                                                                                                                                                                       Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
Bacteria, Proteobacteria, Alphaproteobacteria, Rhodoba
Rhodobacteraceae, Rhodobacter.
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01-JUN-2003
                                                                                                                                                                                                                            biliverdin chromophore.";
Nature 414:776-779(2001).
                                                                                                                                                                                                                                       biliverdin
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           Bacteriophytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016020; C:membrane; IEA.
GO; GO:0005452; F:inorganic anno exchanger
GO; GO:0006820; F:anion transport; IEA.
InterPro; IPR003020; HCO3_cotranspt.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.9%;
                                                                                                                           Phytochrome
                                                                                                                                                                                                                                                                                                                                                                     20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E8B9F71434C0D363 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                   Karniol B., Vieromic histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 accumulate in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity; IEA
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                                                                                                                                                                                                                                                               Vierstra
                                                                                                                                                                                                                                                                                                                                    Rhodobacterales;
                                                                                                                                                                             DNA-dependent; IEA
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                                                                                                                                                                                                                                                    erstra R.
kinases
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; EAL; 1. ; GGDEF; 1.

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Query Match
Best Local Similarity
RESULT 14
QPP8S
ID QPP8S
AC QPP8S
DT 01-MA
DT 01-OC
DE HYPOT
GN YGBM.
OS Esche
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RM (1)
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Q90710
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Best Local
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                                                                                                                                                                                                                                            Q9F8S0;
Q9F8S0;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-CCT-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90710;
01-NOV-1996
01-NOV-1996
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKINLD; FACELOT, TIGRO0834; ae; 1.
TIGRAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE TO THE TO THE TO THE TOTAL TO THE TOTAL TO THE TOTAL TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005452; F:inorganic anion exchanger GO; GO:0006820; P:anion transport; IEA. InterPro; IPR001717; Anion exchange. InterPro; IPR003020; HCO3 cotranspt. pfam; PF00955; HCO3 cotransp; 1. PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Variant AE2 anion exchanger transcripts accumulate types in the chicken gastric epithelium.";
J. Biol. Chem. 271:8895-8902(1996).
EMBL; U48899; AAC59881.1;
HSSP, P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformss; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Proventriculus;
MEDLINE=96224107; PubMed=8621532;
Cox K.H., Adair-Kirk T.L., Cox J.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE2-1 anion
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                                                                                                                                                                                                  Hypothetical YGBM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                               Bacteria; Proteobacteria;
Enterobacteriaceae; Eschei
                                                                                                                                                                    Escherichia coli
                                                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFEPHGYLLTAAVSPGK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPHGYLLTAAVSPG
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                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.9%;
                                                                                                      Escherichia
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                                                                                                                                Gammaproteobacteria; Enterobacteriales;
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Pred. No. 1.2e
0; Mismatches
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Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                             258
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1.2e+02;
ches 5;
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SEQUENCE FROM N.A.

Search completed: March Job time : 5.62201 secs

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RESULT 15
Q9F8R
AC Q9F8R
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DT 01-MA
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Matches 10
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Best Local (
                                                                                                                                                                                                                                                                         MEDLINE=20444184; PubMed=10986240;
Herbelin C.J., Chirillo S.C., Melnick K.A., Whi
"Gene Conservation and Loss in the mutS-rpoS Ge
Pathogenic Escherichia coli.";
J. Bacteriol. 182:5381-5390(2000).
EMBL, AF242209; AAG14976.1; -.
GO:0003677; F:DNA binding; IEA.
GO: GO:0003677; F:DNA binding; IEA.
GO: GO:0004519; F:endonuclease activity; IEA.
GO: GO:0004519; F:DNA repair; IEA.
GO: GO:0006281; P:DNA repair; IEA.
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01-MAR-2001
01-MAR-2001
01-OCT-2003
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J. Bacteriol. 182:5381-5390(2000).
EMBL; AF242208; AAG14970.1; ...
GO; GO:0005522; C:intracellular; IEA.
GO; GO:0003677; F.DNA binding; IEA.
GO; GO:0004519; F:endonuclease activity;
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Hypothetical protein.
SEQUENCE 258 AA; 29218 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0006281; P:DNA repair; IEA.
InterPro; IPR001719; AP_endnuclease2.
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MEDLINE=20444184; PubMed=1098
Herbelin C.J., Chirillo S.C.,
                                                                                                                                                                                                        InterPro; IPR001719; AP_endnuclease2.
Pfam; PF01261; AP_endonuc_2; 1.
Hypothetical_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria;
Encerobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
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131
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                                                                                                                   Similarity
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                                           DAFEPHG-YLLTAAVSPG 17
DRFAPHGKRILVEALSPG
                                                                                                                                                                                       258 AA;
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### ALIGNMENTS

#### canine; veterinary; antibody; vaccine; immunisation. Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fel AAY52515; AAY52515 standard; peptide; 18 28-OCT-1999. WO9954349-A2 Dermatophagoides farinae. House dust mite allergen protein (map) A/B fragment map(5). 22-FEB-2000 16-APR-1999; (first entry) 99WO-US008524 8 diagnosis; human; feline;

17-APR-1998; 13-MAY-1998; 02-SEP-1998; 98US-00062013. 98US-0085295P. 98US-0098909P.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, 臣;

WPI; 2000-052700/04.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Claim 3; Page 69; 154pp; English.

Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWM nemposition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgB present in mite-allergic dog antisera. The HMW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines,

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Query Match
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humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins

តិនិតិនិតិនិង្គ S Matches Query Match Best Local ( Sequence 18 AA; 18; 4.4 Similarity DAFEPHGYLLTAAVSPGK 18 Conservative 100.0%; 0 Score 96; DB 3; Pred. No. 1e-09; Mismatches ω --0, Length 18; Indels 0 Gaps

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μ.

DAFEPHGYLLTAAVSPGK 18

AAU96319 standard; peptide; 18 Ä

AAU96319;

15-JUL-2002 (first entry)

Der HMW-map polypeptide #6

Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.

Dermatophagoides farinae

WO200222807-A2

21-MAR-2002

14-SEP-2001; 2001WO-US028730

14-SEP-2000; 2000US-00662293

(HESK-) HESKA CORP

Mccall CA, Hunter SW,

WPI; 2002-351888/38

New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.

Claim 12; Page 70; 161pp; English.

RESULT 2
AAU96319
ID AAU9
XX AAU9
XX Der
XX Immu
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XX The invention relates to an isolated mite allergenic protein of CD Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for ellciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, CC cat) susceptible to or having an allergic response to a mite. An CC therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the CC detection of anti-per HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (19% or Der HMW-map protein activity associated with a CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting CC binding of proteins to 19%, to prevent immunocomplex formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU99314-AAU96342

Sequence 18

100.0%; Score 96; DB <u>σ</u> Length 18;

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1 DAFBPHGYLLTAAVSPGK 18
DAFEPHGYLLTAAVSPGK 18
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Matches

18;

Conservative

0

Pred. No. le; ; Mismatches

1e-09; 0

Indels

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0

100.0%;

Best Local Similarity

AAY52525 standard; protein; 536 B

AAY52525;

0

22-FEB-2000 (first entry)

House dust mite (D. farinae) mite allergen protein (map) PDerf98-536

Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgB; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.

Dermatophagoides farinae.

WO9954349-A2

28-OCT-1999.

16-APR-1999; 99WO-US008524.

17-APR-1998; 13-MAY-1998; 02-SEP-1998; 98US-00062013. 98US-0085295P. 98US-0098909P.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber ĘŖ

2000-052700/04

N-PSDB; AAZ38579, AAZ38580.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Claim Page 125-127; 154pp; English

This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-536, the mature form of PDerf98-555 (AAX52523). PDerf98-536 chas a molecular weight of 98 kD, comprising 536 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each creation being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. Mite allergenic proteins and populations to modify an animal's hypersensitivity reaction to mite compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to disgnose allergies via a skin test. The proteins and peptides can also be used to they can be used as vaccines to passively immunise animals as spainst dust mite hypersensitivity, as positive controls in test kits and as tools to crecover desired dust mite allergens from a mixture of proteins

Sequence 536 AA;

Matches Query Match Best Local ( 18 Similarity 100.0%; . • Score 96; Pred. No. Mismatches DB 3; 1 6.7e-08; 0 Length 536; 0; Gaps

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166

15-JUL-2002 AAU96329;

(first entry)

AAU96329 standard; protein; 536 AA

22-FEB-2000

(first entry)

dust mite (D.

farinae) mite allergen protein (map) PDerf98-555.

human; feline;

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RESULT 5
AAY52523
ID AAY5
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AC AAY5
XX
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                                                                                                                                                                                                                                                                           The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a nonprotein account epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. At an iterapeutic composition is useful for desentifying an animal to an therapeutic composition is useful for desentitioning a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-per HMW-map partician activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 or represent Der HMW-map polypeptides of the invention
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 125-127; 161pp; English.
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                 AAY52523
                                              AAY52523 standard; protein; 555
                                                                                                                                                                                                                                                   Sequence 536
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DB; ABK69575.
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18; Conserv
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hes 0;
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RESULT 6
AAU96327
ID AAU9
XX

AAU96327 standard;

protein;

555

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                                                                                                                                                                CC (map) PDerf98-55. PDerf98-55 has a molecular weight of 98 kD.
CC comprising 555 amino acids, and is a component of the Dermatophagoides
CC composition. The HMW-map composition was isolated from a D. farinae
CC composition. The HMW-map composition was isolated from a D. farinae
CC composition. The HMW-map composition was isolated from a D. farinae
CC composition. The HMW-map composition was isolated from a D. farinae
CC composition. The HMW-map composition was isolated from a D. farinae
CC composition. The HMW-map composition was isolated from a D. farinae
CC composition. The HMW-map composition being analysed for the
CC presence of proteins that bound to 19% present in mitte-allergic dog
CC composition was be used in therapeutic compositions to modify an
CC canimal's hypersensitivity reaction to mite allergens. Animals that may be
CC treated include mammals and birds, especially felines, canines, equines,
CC thumans, other pets, and work or domestic animals. The proteins or
CC that the control of petiles can also be used to raise antibodies, which have a
CC variety of potential uses. For example, they can be used as vaccines to
CC passively immunise animals against dust mite hypersensitivity, as
CC positive controls in test kits and as tools to recover desired dust mite
CC allergens from a mixture of proteins
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13-MAY-1998;
02-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ38575,
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                                                                                                                                     Sequence 555 AA;
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 185 DAFEPHGYLLTAAVSPGK 202
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                                DAFEPHGYLLTAAVSPGK 18
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                                                                   Conservative
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98US-0085295P.
98US-0098909P.
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/note= "Mature PDerf98-555"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Signal peptide"
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                                                                                100.0%;
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                                                                   Score 96; DB 3;
Pred. No. 7e-08;
); Mismatches
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                                                                                                     DB 3;
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RESULT 7
AAU96328
ID AAU9
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AC AAU9
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DE Der
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KW Der
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated mite allergenic protein of CD Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-protein activity and protein an interpretation of protein and ite. A composition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A composition is useful for desentitising a host animal to an allergic response to a mite. The DNA and protein can be used in the context of anti-Der HMW-map analysististis and inhibition of immunoglobulin (Ig) or Der HMW-map protein activity associated with a context of immunoglobulin (Ig) or Der HMW-map protein activity associated with a context of immunoglobulin (Ig) to provent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 or represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 555 AA;
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                                mite allergenic protein; immunoglobulin immunocomplex formation.
                                              Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                  Der HMW-map polypeptide #15.
                                                                                                                                   15-JUL-2002
                                                                                                                                                                      AAU96328;
                                                                                                                                                                                                     AAU96328 standard; protein; 555
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l Similarity 100.0%;
18; Conservative (
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Pred. No. 7e-
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7e-08;
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CC represent Der HMW-map polypeptides of the invention
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Best Local :
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                                                                                                                                                                                                                                                                                 Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
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Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490
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22-FEB-2000
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                                                                                                                                                                                                                         Dermatophagoides pteronyssinus.
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Pred. No. 7e-08;
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Modified-site

240. .242 /note= "As 115. .117

"Asn is N-glycosylated"

Modified-site

Location/Qualifiers

'note= "Asn is N-glycosylated"

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AAU96339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490 Chas a molecular weight of 98 kD, comprising 490 amino acids, and has a chigh degree of homology with the D. Farinae mature 98 kD allergen, maps CC (AAY52525). Nucleic acid molecules encoding PDerp98-490 were isolated CC from a D. pteronyssius cDNA library by hybridisation with a probe CC encoding the D. farinae high molecular weight map (HMW-map) composition. CC Mite allergenic proteins and peptides, and nucleic acids encoding them, cc may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, cother pets, and work or domestic animals. The proteins or fragments may cother pets, and work or domestic animals. The proteins and cother pets, and work or domestic animals. The proteins and cother pets, and work or domestic animals which have a variety of cotherital uses. For example, they can be used as vaccines to passively controls in test kits and as tools to recover desired dust mite allergens from a control of composition of the protein from a control of the protein and controls in test kits and as tools to recover desired ust mite allergens from a control of the protein from the protein from a control of the p
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13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                           Der HMW-map; American house dust mite; antiallergic; mite; mite allergenic protein; immunoglobulin E; hypersensitivity immunocomplex formation.
14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Der HMW-map polypeptide #26
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98US-0085295P.
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Pred. No. 1.1e-05;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                     E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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AAY52533
ID AAY52
XX AAY52
XX AAY52
XX O6-AU
DT 06-AU
DT 22-FE
XX Mite
XX Mite
XX Mite
XX House
XX Canin
XX Derma
XX Key
FT Pepti
FT Pepti
FT Prote
XX W0995
XX W0995
XX 11-AP
PR 11-AP
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-protein account epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. At the the transmitter of the transmitter of the transmitter of the transmitter of the DMA and protein can be used in the callergic response to a mite. The DMA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig) 3 or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgB, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                       Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                            D. pteronyssius 98 kD mite allergen protein (map) PDerp98-509
                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-2003
22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY52533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 490 AA;
                                                                                                    WO9954349-A2
                                                                                                                                                      Protein
                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                         Dermatophagoides pteronyssinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY52533 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 144-146; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-351888/38.
N-PSDB; ABK69585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-2000; 2000US-00662293
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                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                    /note= "Signal peptide"
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 509
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                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                      .509
                                                                                                                                      "Mature PDerp98-509"
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; Pred. No. 1.1e
1; Mismatches
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17-APR-1998; 16-APR-1999; 28-OCT-1999

99WO-US008524. 9808-00062013

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein (map) pDerp98-509. PDerp99-509 has a molecular weight of 98 kD, comprising 509 amino acids, and has a high degree of homology with the D. farinae 98 kD allergen, maps (AAY22523). Nucleic acid molecules encoding PDerp98-509 were isolated from a D. pterponyssius cDNA library by PDerp98-509 were isolated from a D. pterponyssius cDNA library by the protein acids encoding the D. farinae high molecular weight C map (HMW-map) composition. Wite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines. Animals craimes, equines, humans, other pets, and work or domestic animals. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite cover desired dust mite allergens from a mixture of proteins. (Updated con 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                           Der HMW-map; American house dust mite; antiallergic; mite; I mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 509 AA;
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                                                                                                                                                                    WO200222807-A2
                                                                                                                                                                                                 Dermatophagoides farinae
                                                                                                                                                                                                                                                                                           Der HMW-map polypeptide #24.
                                                                                                                                                                                                                                                                                                                          15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                     AAU96337 standard; protein; 509 AA
               Mccall CA,
                                                                           14-SEP-2000; 2000US-00662293
                                                                                                        14-SEP-2001; 2001WO-US028730
                                                                                                                                        21-MAR-2002
                                                                                                                                                                                                                               immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HESK-) HESKA CORP
                                             (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 134-136; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAFEPHGYLLTAAVSPGK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAFEPFGYLLTAAVSPGK 202
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                 Hunter SW,
                                                                                                                                                                                                                                                                                                                          (first entry)
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98US-0098909P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weber ER;
                 Weber ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 83; DB 3;
Pred. No. 1.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 509;
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AAU96338

III AAU9

XX

AC AAUS

XX

DE DET

XX

DE DET

XX

MO20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dermatophagoides, designated Der HMW-map protein, and its related nucleic control of the Der HMW-map protein is useful for eliciting an immune response control of the Der HMW-map protein. The protein or a reagent comprising a nonce protein accoust epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A composition is useful for identifying an animal to an control of anti-Der HMW-map anti-Doubles in animal funds, and inhibition of anti-Der HMW-map anti-Doubles in animal funds, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a control of immunoglobulin to IgE, to prevent immunocomplex formation, thus control of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 crepresent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 16
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N-PSDB; ABK69581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
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                                                                                                                                                                                                                                                 WPI; 2002-351888/38
N-PSDB; ABK69583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Der HMW-map polypeptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2002
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                                                                                                                                                      New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                   Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                 (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 EAFEPFGYLLTAAVSPGK 202
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                                                                                                                                                                                                                                                                                                                                                   Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.5%;
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Pred. No. 1.2e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic

Claim 12; Page 139-141; 161pp; English.

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RESULT 13
ABP72624
ID ABP72624
XX ABP72624
AC ABP72
XX ABP72
XX ABP72
XX ABP72
XX ABP72
XX Insec
CX Marsu
XX Insec
KW neuro
OS Marsu
XX MO200
XX MASSU
XX O8-AU
XX O8-AU
XX O8-AU
XX O8-AU
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Best Local S
Matches 16
The present sequence is that of prawn (Penaeus japonicus) chitinase. This protein can be used in claimed fusion proteins of the invention comprising a translocating moiety and a toxic molety, where the translocating moiety is a plant protein (e.g. a lectin) capable of acting as a carrier to translocate the toxic moiety across the gut wall of a plant pathogen, and the toxic moiety is an arthropod-derived peptide or protein capable of causing deleterious effects on growth, development, reproduction or mortality in pest insects. Suitable arthropod peptides and proteins include allatostatins, chitinase, diuretic hormone and their metabolites and analogues. Polynucleotides encoding the fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease. Antibodies that bind to bet annouse interpretation, thus binding of proteins to 1gE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting disease. Antibodies that bind to Der HMW-map are useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein useful for combating insect pests, comprises a translocating moiety comprising a plant protein capable of acting as carrier to translocate toxic moiety inside plant pathogen, and a toxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gatehouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYDU-)
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11-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;
neuropeptide; transgenic plant; crop protection; prawn.
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ENVIRONMENT FOOD & RURAL AFFAIRS
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Pred.
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RESULT 14
ABB66399
ID ABB66
XX ABB66
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                                                                                                                                              Query Match
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                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                  Sequence 508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 25989; 21pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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11-JUL-2000;
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294 AFOPRGLILSAAVSPNK
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12; Conserv
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                                                AFEPHGYLLTAAVSPGK 18
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                                                                                                   Conservative
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2000US-00614150.
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2; Mis
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3; Mismatches
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                                                                                                                                              Length 508
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ABP72634 standard; protein; 467 AA.

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RESULT 15
ABP72634
ID ABP72634
ID ABP72634
AC ABP72
XX ABP72
XX ABP72
XX ABP72
XX ABP72
XX PT 11-JU
XX Insec
KW Insec
KW Insec
KW Neuro
XX Marsu
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                                                                                                                                                                                                                                                                                                                     The present sequence is that of prawn (Penaeus japonicus) chitinase. This protein can be used in claimed fusion proteins of the invention comprising a translocating moiety and a toxic moiety, where the translocating moiety is a plant protein (e.g. a lectin) capable of acting as a carrier to translocate the toxic moiety across the gut wall of a plant pathogen, and the toxic moiety is an arthropod-derived peptide or protein capable of causing deleterious effects on growth, development, reproduction or mortality in pest insects. Suitable arthropod peptides and proteins include allatostatins, chitinase, diuretic hormone and their metabolites and analogues. Polynucleotides encoding the fusion protein, vectors, host cells and transgenic plants that are resistant to disease are also provided. The fusion protein is target-specific, and resists cdegradation in the insect gut. (Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                     Matches
                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein useful for combating insect pests, comprises a translocating moiety comprising a plant protein capable of acting as a carrier to translocate toxic moiety inside plant pathogen, and a toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-278469/27.
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neuropeptide; transgenic plant; crop protection; prawn.
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11-JUN-2003
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                                                                                                                                                                                                                                                                Sequence 467 AA;
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(ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
150 ALQPEGMLLTAAVSAGK 166
                                                                                                                                 l Similarity
12; Conserv
                                                               2 AFEPHGYLLTAAVSPGK 18
                                                                                                                                 59.4%; ilarity 70.6%; Conservative
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                                                                                                                                                               Score 57; DB 6;
Pred. No. 0.39;
                                                                                                                                        Mismatches
                                                                                                                                     4.
                                                                                                                                                                                             Length 467;
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Search completed: March 22, 2004, 06:51:40 Job time: 7.47304 secs

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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                Score
                                                            43.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1: /cgn2 6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2 6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2 6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2 6/ptcdata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2 6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2 6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2 6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*
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Match
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Maximum Match 100%
Listing first 45 summaries
                                                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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/ Cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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14 US-10-218-743-6
14 US-10-218-743-15
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14 US-10-218-743-18
14 US-10-218-743-18
15 US-10-218-743-34
16 US-10-218-743-38
17 US-10-369-493-17892
18 US-09-729-674-122
19 US-09-729-674-122
10 US-09-729-674-125
11 US-10-424-596-16
12 US-10-424-599-237149
14 US-10-291-253A-13
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Sequence 6, Appli
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 41, Appl
Sequence 35, Appl
Sequence 37, Appl
Sequence 17892, A
Sequence 17892, A
Sequence 17, Appl
Sequence 17, Appl
Sequence 3125, Appl
Sequence 3125, Appl
Sequence 3125, Appl
Sequence 3125, Appl
Sequence 317, Appl
Sequence 317, Appl
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US-10-218-743-6

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737-149-2	-10-038-854	-10-225-	-10-149-819-2	82-1	-09-930-512-	-10-425-114-6284	25-114-612	-114-612	0-425-114-6124	-114-642	0-282-122A-68	-925-300-157	47-31	-10-673-098-2	-10-671-134-20	US-10-670-844-206	-10-671-419-20	71-403-2	4-099F-5	u	0-424-599-1591	54-24	-69	-10-092-900A-	0-389-566-44	-10-198-070-11	-10-156-761-93	24-599-27	93-2
29,	equence 67,	e 65	Sequence 21, Appl	e 486	e 75, App	e 62846,	e 61243,	e 61242,	on on	e 64200,	ce 68332,	1577, Ap	e 3129	e 206	e 206	equence 206	e 206	e 206	equence 57,	e 207	equence 1591	æ	e 9000,	e 334,	e 440,	Ø	e 9331,	e 279804	equence 23463

#### ALIGNMENTS

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PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 18
TYPE: PRT
ORGANISM: Dermatophagoides farinae
US-10-218-743-6
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 09/062,013
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: AL-2-C3
                                                                                                      Local Similarity
                                                                                 18;
                                    1 DAFEPHGYLLTAAVSPGK 18
DAFEPHGYLLTAAVSPGK 18
                                                                                    Conservative
                                                                                                      100.0%; Score 96; DB 14; 100.0%; Pred. No. 6.1e-09;
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                                                                                    Mismatches
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; LENGTH, 555
TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-15
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION DATE: 1998-04-17
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PRIOR FILING DATE: 1999-04-15

PRIOR APPLICATION NUMBER: 60/098,909

PRIOR TILING DATE: 1998-09-02

PRIOR PELICATION NUMBER: 60/085,295

PRIOR FILING DATE: 1998-05-13

PRIOR APPLICATION NUMBER: 60/098,565

PRIOR FILING DATE: 1998-04-17

PRIOR APPLICATION NUMBER: 09/062,013

PRIOR APPLICATION NUMBER: 09/062,013

PRIOR APPLICATION NUMBER: 09/062,013

PRIOR FILING DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MCCall, Catherine A.
APPLICANT: Hunter, Shirley Mu
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: AND USES THEREOF
FILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
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Publication No. US20030096779A1
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Sequence 15, Application US/10218743
Publication No. US20030096779A1
                                                                                                             NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
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ORGANISM: Dermatophagoides farinae
.10-218-743-21
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CURRENT FILING DATE: 2002-08-13
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Meber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
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APPLICANT: MCGAll, Catherine A.

APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.

ITILE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 2002-08-13
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-03
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
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SEQ ID NO 18
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Best Local 9
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Sequence 41, Application US/10218743
Publication No. US20030096779A1
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PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERWATOPHAGOIDES NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
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CURRENT FILING DATE: 2002-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 DAFEPHGYLLTAAVSPGK 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 96; DB 14; llarity 100.0%; Pred. No. 2.9e-07; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 09/062,013 PRIOR FILING DATE: 1998-04-17

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-218-743-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR PELICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
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SEQ ID NO 41
LENGTH: 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/10218743
Publication No. US20030096779A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine M.
APPLICANT: McCall, Catherine M.
APPLICANT: McCall, Catherine M.
APPLICANT: McCall, Catherine McC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILLING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILLING DATE: 1999-04-15
PRIOR FILLING DATE: 1999-04-15
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 49
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88.9%;
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88.9%; Pred. No. 3.7e-05;
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Pred. No. 3.6e-05;
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US-09-729-674-122

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth APPLICANT: McCoy, John M.

McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.

APPLICANT

Merberg, David Treacy, Maurice Agostino, Michael

Evans, Chery

Steininger II, Robert Spaulding, Vikki Wong, Gordon G.

PPLICANT

sequence 122, Application US/09729674
Patent No. US20010039335A1

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                                                                                                                                                       US-10-369-493-17892
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17892
LENGTH: 375
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Best Local Similarity
                                                                           Matches
                                                                                           Query Match
Best Local 9
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Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                         TYPE: PRT
ORGANISM: SPHINGOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 509
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215 NAFHPYGVLIHAAVDVG 231
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                                   1 DAFEPHGYLLTAAVSPG 17
                                                                                               Similarity
                                                                             Conservative
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                                                                                             49.0%; Score 47; DB 58.8%; Pred. No. 24;
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Pred. No. 3.7e-05
                                                                               Mismatches
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TITLE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM FILE REFERENCE: 6055-64%
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 122
LENGTH: 140
TYPE: PDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 10448-048001

CURRENT APPLICATION NUMBER: US/09/844,948

CURRENT FILING DATE: 2001-04-24

PRIOR APPLICATION NUMBER: US 60/200,604

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

SEQ ID NO 5
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Best Local Similarity
Thes 7; Conserva
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; ORGANISM: Homo sapiens
US-09-729-674-122
                                                                                                                                                                                           US-10-080-960-16
Sequence 16, Application US/10080960; Publication No. US20020197695A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09844948
Publication No. US20030119161A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
APPLICANT: Williamson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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FILE REFERENCE: 38155-20044.00
CURRENT APPLICATION NUMBER: US/10/080,960
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,040
PRIOR FILING DATE: 2000-10-20
                                                                                           APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Glucksmann, Maria
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 80090, 52874,52880,63497,
TITLE OF INVENTION: METHODS AND COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 502
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: 32132, A NOVEL FUCOSYLTRANSFERASE FAMILY ITLE OF INVENTION: MEMBER AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                         229 DAFHPYGYLEPLTA 242
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                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
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71.4%;
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Pred. No. 17;
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Pred. No. 1.1e+02;
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OF HUMAN PROTEINS AND USES THEREOF
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US-10-094-749-3125

GENERAL INFORMATION:

TAKAO

APPLICANT: APPLICANT: ISOGAI,

APPLICANT: PPLICANT:

SUGIYAMA, TOMOYASU OTSUKI, TETSUJI WAKAMATSU, AI SATO, HIROYUKI ISHII, SHIZUKO

APPLICANT: APPLICANT: Sequence 3125, Application US/10094749 Publication No. US20030219741A1

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片
                                                                                                                                                            ; TYPE: PRT ; ORGANISM: Thermococcus hydrothermalis US-10-422-536-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-422-536-17
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SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 16
                                                                                                                                                                                                                                         SOFTWARE: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Applica Publication No. US20 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                             Query Match 45.3%; Score 43.5; Best Local Similarity 47.6%; Pred. No. 9 Matches 10; Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/242,038
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241,992
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,637
PRIOR APPLICATION NUMBER: US 60/242,637
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bennett, Mark
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC
TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: A-71433-1/AMP/CYO
CURRENT APPLICATION NUMBER: US/10/422,536
CURRENT FILING DATE: 2003-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kinsella, APPLICANT: Lorens,
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 168
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 10/232,758 PRIOR FILING DATE: 2002-08-30
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/187,130 PRIOR FILING DATE: 2000-03-06 PRIOR APPLICATION NUMBER: US 09/800,770 PRIOR FILING DATE: 2001-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 502
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Consensus amino acid sequence
                                                                                                                                                                                                                        ENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 71.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 DAFHPYGYLEPLTA 242
84 DVTEDHSLIGYMNTSKVKPGK 104
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                                                                                                                                                                                                                                                                PatentIn version 3.2
                                     DAFEPH---GYLLTAAVSPGK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pray, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10422536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US20040014100A1
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 13;
Pred. No. 1.1e+02;
                                                                                 Mismatches
                                                                                                      96
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                                                                                 Indels
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APPLICANT: TAMECHIKA,
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/01.60
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3125
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-3125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-10-424-599-237149
; Sequence 237149, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_56170C.1.pep US-10-424-599-237149
                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 237149
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                                                                            Matches
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                    FEATURE:
NAME/KEY: unsure
LOCATION: (1).. (305)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                ENGTH: 305
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Local Similarity 57.1%;
tes 8; Conservative
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32 SFLTSGYVLTATGSPG 47
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                                      2 AFEPHGYLLTAAVSPG 17
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHI
                                                                          Conservative
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                                                                                          44.8%; Score 43; DB 12; Length 305; 56.2%; Pred. No. 88;
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Pred. No. 62;
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; TYPE: PRT ; ORGANISM: Meloidogyne incognita US-10-291-253A-13
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                                                                                                                                      Query Match
Best Local Similarity
Thes 9; Conserva
Job time : 3.68205 secs
                  Search completed: March 22, 2004, 07:45:48
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/291,253A CURRENT FILING DATE: 2003-03-31 PRIOR APPLICATION NUMBER: PR8706 PRIOR FILING DATE: 2001-11-07 PRIOR APPLICATION NUMBER: PR8802 PRIOR APPLICATION NUMBER: US60/341404 PRIOR APPLICATION NUMBER: US60/341404 PRIOR FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-291-253A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/10291253A
Publication No. US20030150017A1
GENERAL INFORMATION:
APPLICANT: Botella, Jose
APPLICANT: Graham, Michael
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Fairbairn, David
TILE OF INVENTION: A Method for Facilitating Pathogen Resistance
                                                                                                                                                                                                                                                                                               ENGTH: 318
                                                                           241 ÁFSPNRÝWICAAVGP 255
                                                                                                                AFEPHGYLLTAAVSP 16
                                                                                                                                                    44.8%; nilarity 60.0%; Conservative
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Pred. No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
                                                                                                                                                                                                                                                                                   seq length: 0 seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                 389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
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Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	o.	ហ	4	ω	N	1	Result No.
									39				40	40	41.5	42	43	43.5	45	83	83	83	96	96	96	96	Score
40.6		.0	.0				0		40.6			۳	41.7	41.7	ω	ω	4.	'n	ტ	86.5	9	σ,	00.	00.		00.	Query
 350	318	318	318	318	283	280	105	31	31	31	31	583	354	292	459	207	442	391	309	509	509	490	555	555	536	18	Length
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8-828-	8-487-072A	73-089-3	-08-477-346-3	-08-190-802A-	-266-965-1	9-323-998E-	34-000C-35	-08-487-072A-	-08-473-08	77-346-1	-08-190-802A-1	-09-489-039A-139	-09-489-039A-865	9-252-991A-1953	89-039A-126	-09-489-039A-9	52-778-	-09-800-170-1	89-039A-	ů	92-225-	-09-292-225-4	-09-292-225-	9-292-225-1	-09-292-225-2	92-225-	IU
equence 1,	equence 33,	Sequence 33, Appl	equence 33,	933,	equence 109	equence 37,	equence 356	equence 104, Ap	e 104, Ap	equence 104, Ap	equence 104,	equence 13918,	quence 8658, A	equence 1953	e 12641,	equence 9124, A	equence 2, 1	equence 17,	e 1353	equence 38	nce 35,	equence 41,	e 18, App	equence 15,	e 21,	~	Description

45	44	43	42	41	40	39	38	37	36	35	34	ယ	32	31	30	29	28
38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	9	39	9	9	39	3 9	39	39
40.1	40.1	40.1	40.1	40.1	40.1	40.1	40.1	40.1	40.1	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6
1068	1068	681	681	681	666	666	666	526	127	1179	981	938	713	513	422	414	410
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US-09-113-825-2	US-08-537-210A-2	US-08-532-384-18	US-08-346-128-37	US-08-083-590A-18	US-08-532-384-17	US-08-346-128-36	US-08-083-590A-17	US-09-252-991A-20120	US-09-673-395A-595	US-09-252-991A-17895	US-09-252-991A-16920	US-09-637-145-2	US-09-198-452A-640	US-09-252-991A-19670	US-09-328-352-7491	US-09-252-991A-31156	US-09-540-256-3584
Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	sequence
2, Appli	2, Appli	18, Appl	37, Appl	18, Appl	17, Appl	36, Appl	17, Appl	20120, A	595, App	17895, A	16920, A	2, Appli	640, App	19670, A	7491, Ap	50	3584, AD

# ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
UNMBER: 0F SQD, ID NOS: 49
SOPTWARE: PATENTING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 18
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-09-292-225-6
Sequence 21, Application US/09292225

Patent No. 6455686

PREPAIL INFORMATION:
APPLICANT: MCCall, Catherine A.
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
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                                                                                                                                                                                                                                         US-09-292-225-21
                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09292225 Patent No. 6455686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                            ch 100.0%;
l similarity 100.0%;
l8; Conservative 0;
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Pred. No. 3.3e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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RESULT 4
US-09-292-225-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: McCall, Catherine A.

APPLICANT: Hunter, Shirley Wu

APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3

CURRENT APPLICATION NUMBER: US/09/292,225

CURRENT FILING DATE: 1999-04-15

CURRENT FILING DATE: 1999-04-15

EARLIER APPLICATION NUMBER: 60/098,909
                                                                                             Sequence 18, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 555
TYPE: PRT
ORGANISM: Dermatophagoides farinae
S-09-292-225-15
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SEQ ID NO 21
LENGTH: 536
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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Patent No. 6455686
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Best Local :
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ORGANISM: Dermatophagoides farinae
-09-292-225-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
MINDER FILING DATE: 1998-04-17
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EARLIER APPLICATION NUMBER: 09/062,013
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EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49
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hes 18; Conser
                                                                                                                                                                                                                                                                 185 DAFEPHGYLLTAAVSPGK 202
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RESULT 6 US-09-292-225-35

GENERAL INFORMATION: APPLICANT: McCall,

Sequence 35, Application US/09292225 Patent No. 6455686

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US-09-292-225-41
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US-09-292-225-18
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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LENGTH: 555
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EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
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EARLIER FILING DATE: 1998-04-17
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166 EAFEPFGYLLTAAVSPGK 183
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88.9%; Pred. No. 3.2e-06;
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Pred. No. 2.1e-08;
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-35
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US-09-292-225-38
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 509
TYPE: PRT
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LENGTH: 509
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
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EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1998-04-17
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APPLICANT: Weber, Eric R.
                                                                                                  Local
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185
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16; Conserv
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EAFEPFGYLLTAAVSPGK 202
                                   DAFEPHGYLLTAAVSPGK 18
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ilarity 88.9%;
Conservative
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                                                                           Score 83; DB
Pred. No. 3.4e
1; Mismatches
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Pred. No. 3.4e-06;
1; Mismatches 1
                                                                                              3.4e-06;
                                                                                                                     DB 4;
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                                                                                                                   Length 509;
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RESULT 8 US-09-489-039A-13534 ; Sequence 13534, Application US/09489039A

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APPLICANT: Bryant, Peter J.
APPLICANT: KAWAMUYA, KAZUO
ITILE OF INVENTION: CHTINASE RELATED PROTEINS AND
ITILE OF INVENTION: OF USE
FILE REFERENCE: 07306/015001
CURRENT APPLICATION MOMBER: US/09/052,778A
CURRENT FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Thermococcus hydrothermalis US-09-800-170-17
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PURCHER FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13534
LENGTH: 309
TYPE: PRT
                                                                                                                                                                                                                                                    Sequence 2, Application US/09052778A Patent No. 6060590 GENERAL INFORMATION:
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Best Local Similarity 56.2%;
Matches 9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kinsella, Todd
TITLE OF INVENTION: IN VIVO PRODUCTION OF
FILE REFERENCE: A-68614-1/DJB/RMS/RMK
TYPE: PRT
ORGANISM: Drosophila melanogaster
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Pred. No. 1
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Query Match
Best Local Similarity
Thes 9; Conserve
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                             RESULT 13
US-09-252-991A-19532
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US-09-489-039A-9124
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Best Local S
Matches 8
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PROLUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 12641 LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9124, Application US/09489039A Patent No. 6610836
Sequence 19532, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gary Br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12641, Application US/09489039A Patent No. 6610836
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LENGTH: 207
                                                                                                                                                                           Matches
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CURRENT APPLICATION NUMBER: US/09/489,035
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae
-09-489-039A-12641
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GAZY BREEON Et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Klebsiella pneumoniae
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les 8; Conserv
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9; Conserve
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Pred. No.
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Pred. No. 15;
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Pred. No. 4
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26;
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SEQ ID NO 13918 LENGTH: 583 TYPE: PRT

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FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19532
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                                                                                                                                                                                                                                                    US-09-489-039A-13918
                                                                 GENERAL INFORMATION:

GENERAL HOROMATION:

APPLICANT: Gary Breton et. al

APPLICANT: GARY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA,

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FITLE REFERENCE: 2709.2004001

FITLE REFERENCE: 2709.2004001
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LENGTH: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8658, Application US/09489039A Patent No. 6610836
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Best Local
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION UNMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gary Breton et al TITLE OF INVENTION: NUCLERIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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8; Conservative
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8; Conserv
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nilarity 44.4%;
Conservative :
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Pred. No.
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Pred. No. 52;
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Search completed: March 22, 2004, 07:03:55 Job time : 1.45081 secs	Qy 8 YLLTAAVSPG 17       :    Db 547 YLLTAAISAG 556	Query Match 41.7%; Score 40; DB 4; Length 583; Best Local Similarity 80.0%; Pred. No. 1.2e+02; Matches 8; Conservative 1; Mismatches 1; Indels	ORGANISM: Klebsiella pneumoniae US-09-489-039A-13918
		Length 583;	
		0;	
		0; Gaps	
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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T19111
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Query Match
Best Local S
Matches 9
                                             Genetics:
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h 71.9%;
Similarity 69.2%;
9; Conservative
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#### ALIGNMENTS

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1484 <GRA>
A;Cross-references: EMBL:U70858; PIDN:AAB09177.1; GSPDB:GN00023; CESP:T01C4.1
A;Experimental source: strain Bristol N2; clone T01C4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 60/1; 179/1; 219/3; 392/3; 481/3; 549/2; 594/2; 736/3;
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A; Accession: T29275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, September 1996 A; Description: The sequence of C. elegans cosmid T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T01C4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-617 < NHA>
                                                                                                                                                                                                                                       submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C04F6.
A;Reference number: Z18346
A;Accession: T15408
                                                                                                                                                     A;Cross-references: EMBL:U42835; NID:g1125760; PID:g1125762; PIDN:AAA83586.1; CESP:C04F6
                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDB:
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Matches 8; Conserv
                                                                                    CESP:C04F6.3
ns: 28/1; 66/2; 504/1
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Score 46; DB:
Pred. No. 2.2;
2; Mismatches
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4; Mismatches
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Indels

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hypothetical protein C08H9.12 - Caenorhabditis elegans C1.Species: Caenorhabditis elegans C.)Species: Caenorhabditis elegans C.)Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19111 #R.L109d, C.
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A;Reference number: Z19838
A;Accession: T24074
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z70035; PIDN:CAA93863.1; GSPDB:GN00020; CESP:R09D1.3 A;Experimental source: clone R09D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-435 <WIL>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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submitted to the EMBL Data Library, A;Reference number: Z19074
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A; Introns: 39/1;
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A; Residues: 1-399 <WIL>
A; Cross-references: EMBL: Z54342; PIDN: CAA91153.1; GSPDB: GN00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T19115
A;Status: preliminary; translated
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Best Local :
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7; Conserve
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Pred. No. 3.6;
                                                                                                                                                                                                                                                                          Score 42; DB 2;
Pred. No. 7.7;
3; Mismatches
                      October
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RESULT 7
T28113
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A;Residues: 1-465 <WIL>
A;Residues: 1-465 <WIL>
A;Cross-references: EMBL:Z54342; PIDN:CAA91151.1; GSPDB:GN00020; CESP:C08H9.4
A;Experimental source: clone C08H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A;Reference number: Z19074 A;Accession: T19113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C08H9.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct 1999 #sequence_revision 15-Oct 1999 #text_change 15-Oct 1999 C;Accession: T19113
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A; Status: preliminary; i
A; Molecule type: DNA
A; Residues: 1-460 < WIL>
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                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A;Reference number: Z20471 A;Accession: T28113
                                                                                                                                                                                                                                                                                                        hypothetical protein ZK938.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28113
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Query Match
Best Local Similarity
"---hes 7; Conserv
                                                                                   A; Map position:
A; Introns: 161/1
                                                                                                                     A; Gene: CESP: ZK938.6
                                                                                                                                      C; Genetics:
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                                                                                                                                                                        A;Cross-references: EMBL:Z49913;
                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-522 <WIL>
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Best Local S
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53.8%;
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Pred. No. 8.9
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Pred. No. 9;
                               Score 42; DB
Pred. No. 10;
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A; Molecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-633 <WIL>
A; Residues: 1-633 <WIL>
A; Cross-references: EMBL: Z66524; PIDN: CAA91419.1; GSPDB: GN00020; CESP: T13H5.3
A; Cross-references: clone T13H5
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text.
C;Accession: S76633
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T;
R;Lightning, J
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N;Alternate names: 1,4-beta-poly-N-acetylglucosaminidase; chitodextrinase
C;Species: Clostridium paraputrificum
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 25-Aug-2003
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A;Accession: T24898
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J. Bacteriol. 179, 7306-7314, 1997
A;Title: Cloning, sequencing, and expression of the gene encoding A;Reference number: Z14138; MUID:98053843; PMID:9393694
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/Species: Caenorhabditis elegans
/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                               ;Genetics:
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Best Local
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glycosidase;
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7; Conserv
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                                                                                         Synechocystis sp.
                                                                                                                                                                                                                                                                                                                      with C-terminal hydrolase
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                                                                                                                                                                                                                                                   Score 42; DB
Pred. No. 16;
4; Mismatches
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 Y.; Miyajima,
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                                                  Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-I, Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AB1452

A; Status: preliminary
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   A; Molecule type: DNA
A; Residues: 1-756 <G:
A; Cross-references: (
                                                                                                                                                                                                                                 chitinase B homolog lin0153 (imported)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision
C;Accession: AB1452
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Dominguez-Bernal, G.; Duchaud, E.; Durand,
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1-756 <GLA>

lin0153 [imported] - Listeria innocua

, C.; Amend, Durand, L.; I

, A.; Baquero, I Dussurget, O.;

F.; Berche, P.; Entian, K.D.;

; Bloecker Fsihi, H.

Kurapkat, G.; Madueno,
, A.; Vazquez-Boland, J.

Þн

Maitournam, Voss, H.; W

m, A.; Ma Wehland,

27-Nov-2001 #text\_change 25-Aug-2003

(strain Clip11262)

B

AL592022;

PIDN:CAC95386.1;

PID:g16412572;

GSPDB:GN00178

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A; Molecule type: DNA
A; Residues: 1-462 < KAN >
A; Cross-references: EMB
A; Note: the nucleotide:
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                                                                                                                           A; Experimental source: C; Genetics: A; Gene: lmo0105 C; Superfamily: chitina:
                                                                                                                                                                                                                                                              A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Warther: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1088
                                                                                                                                                                                 A;Cross-references: GB:NC 003210;
A:Experimental source: strain EGD-
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-756 <GLA>
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Science 294, 849-852,
                                                                                                                                                                                                                                                                                                                                                                                                      R;Glaser,
                                                                                                                                                                                                                                                                                                                                                                                                                                   chitinase B homolog lmo0105 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change
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198
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46.2%;
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was submitted
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                                                                               Score 41;
Pred. No.
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23;
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Fsihi, H.
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A;Experimental source: strain Clip11262 C;Genetics:
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C;Superfamily: chitinase with C-terminal chitin-binding domain
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A;Residues: 1-2819 <SUX>
A;Cross-references: EMBL.AF030693; NID:g2642515; PIDN:AAC47854.1; PID:g2642516
A;Experimental source: strain HB3; from Honduras
                                                                                                                                                                                                                                                                                                                                                                                                                    probable chloroquine resistance protein CG2 (strain HB3) - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000 C;Accession: T09080
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R;Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellems, T.E.

Reju, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellems, T.E.

R;Su, 593-603, 1997

A;Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant A;Reference number: Z16556; MUID:98054002; PMID:9393853

A;Accession: T09079
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                                                                                                                                                                                                                                                                                                                                    ell 91, 593-603, 1997
;Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
;Reference number: Z16556; MUID:98054002; PMID:9393853
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                                                                            Best Loc
Matches
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Best Local
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Local Similarity 46.28;
hes 6; Conservative
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DKONYLNFIKOKK 1237
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pred. No. 86;
3; Mismatches
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RESULT 15

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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: F75551
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Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acyl-CoA-binding protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                           A;Gene: DR0166
A;Map position: 1
C;Superfamily: endozepine; endozepine homology
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Search completed: March 22, 2004, 07:01:26 Job time: 2.84547 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-84 < WHI>
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A;Experimental source: strain Rl
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Matches
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                                                                                                                               2 KONYLALVRELK 13
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                                                                                                                                                                                               62.5%; Score 40; DB 2; 66.7%; Pred. No. 3.7; tive 2; Mismatches
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C.; Maj
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Run

on:

Sequence:

Searched:

OM protein -

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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        protein search, using sw model
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      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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COX6_SCHPO
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YCX2_CYAPPA
MSP1_PLAFPD
BET4_YEAST
SYGA_HELPJ
SYGA_HELPJ
Y591_AQUAE
FX16_MOUSE
FX16_MOUSE
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    066628 aquifex aeo
p75146 mycoplasma
031778 bacillus su
0827d7 streptomyce
p9ak84 streptomyce
p19598 plasmodium
p13819 plasmodium
p13819 plasmodium
p47639 mycoplasma
001007 herpesvirus
008387 saccharomyc
09gx51 mus musculu
09ji55 cricetulus
015149 homo sapien
p30427 rattus norv
p12406 anabaena sp
024174 oryza sativ
p30533 bacillus ci
p27033 bacillus ci
p27033 bacillus co
p24174 cyanophora
p13827 placillus ce
p48324 cyanophora
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056853 aquifex aeo
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2 homo sapien
            InterPro; IFR00123; Glyco_Nydro_18.
InterPro; IFR001279; Glyco_Nydro_18.
InterPro; IFR001279; Glyco_hydro_18AS.
Pfam; PF00507; CEM_14; 2.
Pfam; PF00704; Glyco_hydro_18; 1.
Pr0Dom; PD000471; Glyco_hydro_18; 1.
SMART; SM00494; ChtBD2; 2.
SMART; SM006494; CHTF_BIND_II; 2.
PROSITE; PS01095; CHTTINASE_18; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Repeat.
DOMAIN 478 534 CHITIN-BINDING TYPE-2 1.
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Result No.

Database

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P56287	Q8aab1	051739	P98140	Q8xyl0	Q9x0x6	P57256	045460	Q9h5i1	P75122	Q97w96	P14433
schizosacch	b glucosami	pyrococcus	bos taurus	ralstonia s	t bifunctio	buchnera ap	caenorhabdi	homo sapien	mycoplasma	sultolobus	mus musculu

# ALIGNMENTS

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InterPro; IPR002557; Chitin_bind_PerA.	03923.	PIR; T37249; T37249.	PIR; T15408; T15408.	EMBL; AF026152; AAB81847.1;	EMBL; U42835; AAA83586.1;			entities requires a license agreement (See http://www.isb-sib.ch/announce/	modified and this statement is not removed. Usage by and for commercial	use by non-profit institutions as long as its content is in no way	the European Bioinformatics Institute. There are no restrictions on its	between the Swiss Institute of Bioinformatics and the EMBL outstation -	This SWISS-PROT entry is copyright. It is produced through a collaboration		: Contains 2 chitin-binding type-2 do	hydrolases).	<ul> <li>-!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl</li> </ul>		-i- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-	Insect Mol. Biol. 7:233-239(1998).		"Chitinases are a multi-gene family in Aedes, Anopheles and		MEDITURE OF GATIO FROM M.A. MEDITURE OF GATIO FROM M.A.	DECEMBER OF COLUMN A	SUDMITTED (DEC-1995) to the Embh/Genbank/Dubb Galababes.	(110 100) to the TMT: (2-10-16-70)	STRAIN=Bristol N2;	SEQUENCE FROM N.A.		NCBI TaxID=6239;	Rhabditidae; Peloderinae; Caenorhabditis.	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	Caenorhabditis elegans.		ochitinase (EC	(Rel. 43,	Rel. 35, Last	Creat	4; 017321;	CHIT CAEEL STANDARD; PRT; 617 AA.	CAREL	3

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P36272; P30923;
01-JUL-1993 (Rel. 2
01-JUN-1994 (Rel. 2
10-OCT-2003 (Rel. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Chitinase-3 like protein 1 precursor (Cartilage glycoprotein-39) (GP-39) (39 kDa synovial protein) (YKL-40).
                                                                                                                                                                                                                                                                                                                                 MEDIINE-97386591; PubMed-9244440; Rehli M., Krause S.W., Andressen R.; "Molecular characterization of the gene for human cartilage (CHI3L1), a member of the chitinase protein family and marke late stages of macrophage differentiation."; Genomics 43:221-225(1997).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                       between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as lits content is in no way
modified and this statement is not removed. Usage by and for commercial
entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       Nyirkos P., Golds E.E.;
"Human synovial cells secrete a 39 kDa protein similar to mammary protein expressed during the non-lactating period Biochem. J. 269:265-268(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94064658; PubMed=8245017;
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                                                                                                         This
                                                                                                                                            FUNCTION: May play an important role in the capacity of respond to and cope with changes in their environment. SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: Present in articular chondrocytes, cells as well as in liver. Undetectable in muscle tissu pancreas, mononuclear cells, or fibroblasts.
PTM: Glycosylated.
                                                                                                                                SIMILARITY: Belongs to family 18 of glycosyl hydrolases
                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration -
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EMBL; Y08375; CAA69661.1; J
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005201; F:extracellular space; TAS.
GO; GO:0005201; F:extracellular matrix structural
Interpro; IPR001223; Glyco_hydro_18;
Interpro; IPR001579; Glyco_hydro_18AS.
Pfam; PP00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SNART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
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PDB; 1LA7; 10-APR-02.
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube: Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
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Pred. No. 7.3;
5; Mismatches
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N-LINKED (GLCNAC. . .) (POT)
, 76ADD8298EEEC2D1 CRC64;
     proteome.
06C849B676F6DF01 CRC64;
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Length 403;

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RESULT 4
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                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
PTS system, mannitol-specific IIBC component (EIIBC-
permease IIBC component) (Phosphotransferase enzyme
(EC 2.7.1.69) (EII-Mtl).
MTLA OR MPN651 OR MP191.
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Nucleic Acids Res. 24:4420-4449(1996)
-!- FUNCTION: This is a component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plage:
                                                                                                                                                                                      EMBL; AE000020; AAB95839.1; ALT FRAME. InterPro; IPR003352; Ptrans_EIIC. InterPro; IPR003501; Ptrans_IIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                          Pfam; PF02378; PTS_EIIC; 1. Pfam; PF02302; PTS_IIB; 1. Phosphotransferase system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herrmann R.;
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                                                                                                                                                 Transmembrane;
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L6-OCT-2001 (Rel.
L5-MAR-2004 (Rel.
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Chummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Chummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Chummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Connerton I.F., Chummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Connerton I.F., Chummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Goffeau A., Golightly E.J., Grandi G.,
RA Choi S.K., Codani J., Rogingstein G., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Kurita K., Lapidus A., Ladinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parescan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan B., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan B., Schleich S., Schroeter R., Scoffone F.,
RA Schiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Schight J., Tanaka T., Takahashi H., Takemaru K.,
RA Yoshida K., Yanamoto H., Yanane K., Yasumoto K., Yata K.,
RA Yasumoto K., Yata K.,
RA Yasumoto K., Yata K
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30-MAY-2000
30-MAY-2000
10-OCT-2003
PIR; D69884; D050000.
Subtilist; BG13418; ymcB.
InterPro; IPR006638; Blp3.
InterPro; IPR006463; MiaB_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein ymcB. YMCB OR BSU17010.
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                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
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                                                                                                            p. 299112; CAB13574.1; D69884; D69884.
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(Rel. 42,
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Last annotation updat
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Sakaki Y., Hattori M., Comura S.;

T "Complete genome sequence and comparative analysis of the industrial

IT microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003).

I Nat. Biotechnol. 21:526-531(2003).

The glycine cleavage system catalyzes the degradation of

glycine. The protein binds the alpha-amino group of glycine

through its pyridoxal phosphate cofactor; CO(2) is released and

the remaining methylamine moiety is then transferred to the

lipoamide cofactor of the H protein (By similarity).

C -i-CAPALYTIC ACTIVITY: Glycine + lipoylprotein = S-

-i-CAPALYTIC ACTIVITY: Glycine + lipoylprotein = S-

-i-CAPALYTIC The glycine cleavage system is composed of four proteins:

C -i-SUBUNIT: The glycine cleavage system is composed of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches
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Q827D7;
10-OCT-2003 (Rel. 42, 1
10-OCT-2003 (Rel. 42, 1
10-OCT-2003 (Rel. 42, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glycine dehydrogenase [decarboxylating] (EC 1.4.4.2) (Glycine decarboxylase) (Glycine cleavage system P-protein).
GCVP OR GCVB OR SAV6987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";
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Pfam; PF01938; TRAM; 1.
Pfam; PF00193; UPF0004; 1.
SMART; SM00729; Elp3; 1.
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                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=MA-4680 / A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces avermitilis.
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                                                                               P, T, L and H (By similarity).
SIMILARITY: Belongs to the gcvP family.
          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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DRERYMELVRKIK 356
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nilarity 46.2%;
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IN Nature 417:141-147(2002).

In Indian actino a system catalyzes the degradation of coelic co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentley S.D., Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP005048; BAC74698.1; ALT_INIT. HAMAP; MF_00711; -; 1. InterPro; IPR003437; GDC-P. Pfam; PF02347; GDC-P; 1.
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MEDLINE=21996410; PubMed=12000953;
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                               Tolle R., Bujard H., Cooper J.A.; "Plasmodium falciparum: variations within the merozoite surface antigen1."; Exp. Parasitol. 81:47-54(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-8816657; PubMed=3327688;
Certa U., Rotmann D., Matile H., Reber-Liske R.;
"A naturally occurring gene encoding the major surface antigen
"A recursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence u)
01-NOV-1997 (Rel. 35, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSP1_PLAF3
P19598; Q25921;
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                                                    SIGNAL
CHAIN
TRANSMEM
                                                                                                                        EMBL; M35727; AAA29715.1; ..

EMBL; Y00087; CAA68280.1; ..

EMBL; Z35326; CAA84555.1; ..

InterPro; IPR006209; EGF_11ke.
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Eukaryota; Alveolata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5834;
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                                                                                                     Malaria;
                                                                                                                  Pfam; PF00008; EGF; 1.
                                                                                          [ransmembrane;
                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                               PTM: Merozoite surface antigen contain the sequence of 83 kDa and 19 kDa antigens which are the major surface antige
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                                                                                                    Merozoite; Polyprotein; Repeat;
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Mol. Biochem. Parasitol. 27:291-302(1988)
                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5837;
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                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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Brown G.V., Anders R.F., Kemp D.J
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PIR; A54498; A54498.
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                                                                                                                      Transmembrane;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                      "Variation in the precursor to the major merozoite
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01-AUG-1988 (Rel. 08, Created)
01-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata;
NCBI_TaxID=70153;
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CARBOHYD
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein;
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Tanabe K., Mackay M., Goman M., Scaife J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X05624; CAA29112.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
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M., Goman M., Scaife J.G.;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing.";
J. Bacteriol. 175:7918-7930(1993).
J. Bacteriol. 175:7918-7930(1993).
J. Bacteriol. 175:7918-7930(1993).
I. CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = AMP +
diphosphate + L-tyrosyl-tRNA(Tyr).
I. SUBUNIT: Homodimer (By similarity).
I. SUBUNIT: Homodimer (By similarity).
I. SUBCELLULAR LOCATION: Cytoplasmic.
I. SUBCELLULAR LOCATION: Cytoplasmic.
I. SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
I. SIMILARITY: Contains 1 S4 RNA-binding domain.
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STRALMS-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
Peterson S.M., Hu P.-C., Bott K.F., Hut
"A survey of the Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser C.M., Gocayne J.D., white O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J. Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J. Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403 (1995).
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01-FEB-1996 (Rel. 33, La
28-FEB-2003 (Rel. 41, La
Tyrosyl-tRNA synthetase
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01-FEB-1996 (Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
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                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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Pred. No. 83;
2; Mismatches
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by using
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Kelley J.M.,
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InterPro; IPR002342; S4.
InterPro; IPR002305; tRNA-synt\_ib.
InterPro; IPR001412; tRNA-synt\_I.
InterPro; IPR002307; Tyr\_tRNA-synt\_ib.
Pfam; PF01479; S4; 1.

TIGR; MG455;

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01-APR-1993
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CONFLICT
SEQUENCE
                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
PROSITE; PS50889; S4; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                         EMBL; X64346; CAA45647.1; -. InterPro; IPR004285; UL87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92333688; PubMed=1321287; Albrecht J.-C., Nicholas J., Biller D., Camero Newman C., Wittmann S., Craxton M.A., Coleman
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Gammaherpesvirinae; Rhadinovirus
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SMART; SM00363; S4; 1.
                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BCRF1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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KKNYLRLVSALK 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8B0495F7DFDD738B CRC64;
                                                                                                                                                                                 B6B35F2A8EEBF3D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cameron K.R., Biesinger
oleman H., Fleckenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                Length 731;
                                                                                                                                                                                 CRC64;
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                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biesinger
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                                                                                        0
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RESULT 13
DNL4\_YEAST
ID DNL4\_YEAST

STANDARD;

PRT;

944

Query Match

57.8%;

Score 37;

В

Length 944;

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STEES SOOSO SE REPERE REPERE REPERE POSSOS SOCIO CON LE PRESENTATE DE LA PRESENTATION DE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z74913; (
EMBL; U43491; J
EMBL; U43491; J
PIR; S66870; S
                                                                                                         DNA repair; DNA ATP-binding; Nuc DOMAIN 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae.";
Nucleic Acids Res. 25:1485-1492(1997).
Nucleic Acids Res. 25:1485-1492(1997).
Nucleic Acids Res. 25:1485-1492(1997).
Nucleic Acids Res. 25:1485-1492(1997).
Nucleic Res. 25:1485-1492(1997).
Nucleic Res. 25:1485-1492(1997).
Nucleic Res. 26:1485-1492(1997).
Nucleic Res. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sterky F., Holmberg A., Pettersson B., Uhlen M.; "The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               008387; 002913; Q02914;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA ligase II (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP])
CDNA ligase IV homolog)
DNI4 OR YOROOSC OR UND407 OR UNE452.
                                                                                                                                                                                                               PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatice and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00533; BRCT; 2.
Pfam; PF01068; DNA_ligase; 1.
SMART; SM00292; BRCT; 1.
TIGREAMS; TIGR00574; dnll; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97248602; PubMed=9092653;
Ramos W., Tappe N., Talamantez J., Friedberg E.C., Tomk:
"Two distinct DNA ligase activities in mitotic extracts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which correspond to previously identified genes."; Yeast 12:1091-1095(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
SEQUENCE
                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0003910; F:DNA ligase (ATP) activity;
GO; GO:0006303; P:double-strand break repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GermOnline; 143593; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001357; BRCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S0005531; DNL4
                                                                                                                                                                   PS50172; BRCT; 2.
PS00039; DNA_LIGASE_A1; 1.
PS00339; DNA_LIGASE_A2; 1.
PS50160; DNA_LIGASE_A3; 1.
PS50160; DNA_LIGASE_A3; 1.
PS50160; DNA_LIGASE_A3; 1.
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(JUL-1996) t
   944 AA;
                                        681
840
282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; CAA99193.1;
; AAC49485.1;
; AAC49484.1;
                                                                                                                                          Nuclear
                                        ar protein;
780 B
941 B
282 A
       108514
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he EMBL/GenBank/DDBJ databases
       X
X
                                    n; Repeat.
BRCT 1.
BRCT 2.
BRCT 2.
AMP (BY SIMILARITY).
       7FB6D7927E1719B5 CRC64;
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via nonhomologou.
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                                                                                                                                                                                  Cell
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                                                                                                                                                                                     division;
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RESULT PLE1\_MC

MOUSE

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLEI MOUSE STANDARD; PRT; 964 AA.

Q9QXS1; Q9CS65; Q9QUT2; Q9QXQ8; Q9QXR0; Q9QXR1; Q9QXR2;
Q9QXR3; Q9QXR4; Q9QXR5; Q9QXR6; Q9QXR7; Q9QXR8; Q9QXR9; Q9QXS0;
Q9QXS2; Q9QXS3;
16-OCT-2001 (Rel. 40, Created)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuchs P., Zoerer M., Rezniczek G.A., Spazierer D., Oehler S., Castanon M.J., Hauptmann R., Wiche G.; "Unusual 5' transcript complexity of plectin isoforms: novel tissue-specific exons modulate actin binding activity."; Hum. Mol. Genet. 8:2461-2472(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain, Emb:
MEDLINE=20025755;
                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- FUNCTION: Interlinks intermediate filaments with microtubules and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 181-812 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plectin 1 (PLTN)
                                                                                                                                                                                                           ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=16;
                                                                                                                                                                                                                                                                           scapilization of cytoskeletal intermediate filaments network, also in the regulation of their dynamics.
                                            Name=PLEC-1B, 2A;
                                                                                                                                                                                                                                                             SUBUNIT: Homodimer or homotetramer
                                                                                                                                                                                                                                                                                                                                     microfilaments and anchors intermediate filaments to desmosomes or hemidesmosomes. May be involved not only in the crosslinking and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
                                                                IsoId=Q9QXS1-3; Sequence=VSP_005036, VSP_005045, VSP_005048;
                                                                                                                  IsoId=Q9QXS1-2;
                                                                                                                                                                 IsoId=Q9QXS1-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ., ALTERNATIVE SPLICING, AND TISSUE SPECI
ryo, Heart, Kidney, Skeletal muscle, and
PubMed=10556294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%;
                                                                                                               Sequence=VSP_005048
                                                                                                                                                                 Sequence=Displayed;
                   Sequence=VSP_005037, VSP_005045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment).
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                        intermediate filaments
                                                                                                                                                                                                                                                               (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                             desmosomes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Testis;
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    EMBL; AF188006; AAF18066.1; --
EMBL; AF188007; AAF18069.1; --
EMBL; AF188008; AAF18069.1; --
EMBL; AF188009; AAF18069.1; --
EMBL; AF188010; AAF18070.1; --
EMBL; AF188011; AAF18077.1; --
EMBL; AF188012; AAF18077.1; --
EMBL; AF188013; AAF18077.1; --
EMBL; AF188014; AAF18077.1; --
EMBL; AF188015; AAF18077.1; --
EMBL; AF188016; AAF18077.1; --
EMBL; AF188017; AAF18077.1; --
EMBL; AF188019; AAF18077.1; --
EMBL; AF188019; AAF18077.1; --
EMBL; AF188019; AAF18077.1; --
EMBL; AF188019; AAF18078.1; --
EMBL; AF188019; AAF18080.1; --
EMBL; AF188020; AAF18080.1; --
EMBL; AF188023; AAF18083.1; --
                      Pfam;
Pfam;
                                                                InterPro; IPR001589; Actbind actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR005226; S10_plectin_N.
InterPro; IPR0052217; Spectrin.
IPR0052017; Spectrin.
Pfam; PF00307; CH; 2.
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TISSUE SPECIFICITY: Expressed at high levels in lung, brain, intestine, muscle, heart and skin with lower levels found in kidney, liver, uterus, spleen and salivary gland.

DOMAIN: The N-terminus interacts with actin, the C-terminus vimentin, desmin, GFAP, cytokeratins, lamin B; whereas both and the C-terminus can bind integrin beta-4.

PIM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM INTERMEDIATE FILMMENTS DURING MITOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 actin-binding domain.
SIMILARITY: Contains 2 calponin-homology (CH) domains.
SIMILARITY: Contains 3 spectrin repeats.
SIMILARITY: Belongs to the plakin or cytolinker family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=PLEC-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=PLEC-1E, 2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9QxS1-10; Sequence=VSP_005032, VSP_005041, VSP_005048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9QXS1-9; Sequence=VSP_005032, VSP_005041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9QXS1-8; Sequence=VSP_005039,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9QXS1-5; Sequence=VSP_005037, VSP_005045, VSP_005048, VSP_005048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9QXS1-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9QXS1-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       me=PLEC-0,1C,2A;
IsoId=Q9QXS1-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9QXS1-6; Sequence=VSP_005039, VSP_005047, VSP_005048
                      PF03501; S10_plectin; 1. PF00435; spectrin; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9QXS1-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9QXS1-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9QXS1-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xS1-7; Sequence=VSP_005039;
1C,2A,3A;
                                                                                                                                                                                  Pleci
S10_plectin_N;
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CH 1.
CH 2.
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                                                                                4.
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SPECTRIN 2.
SPECTRIN 3.
                                                                              Score 37; DB Pred. No. 70; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVAGMLMPLDRLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
GVTNLQVMRAMASLKARGLVRETFA -> MSGEDSEVRPVA
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GVT -> MAGTWAAKGVFTSQREVLLERPCWLDGGCEQVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVAGMLMPLDRLRAIYEVLFREGVMVAKKDRRPRSLH
MEPSGSLFPSLVVVGHVVTLAAVWHWRKGHRQAKDEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP_005035.
MVAGMLMPLDRLRAIYEVLFREGVMVAKKDRRPRSLH
MSQHRLRVPEPEGLGSKRTSSEDNLYLAVLRASEGKK
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MVAGMLMPLDRLRAIYEVLFREGVMVAKKDRRP
VCRRKLSPSGSTNTLSRLRGTSVTCTKTS (in
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MVAGMLMPLDRLRAI -
                                                                                                                                                           Missing (In isoform PLEC-0,1C,2A,3A). /FTId=VSP_005047.
                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform /FTId=VSP_005042.
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VLDPAERAVIRIA (in isoform PLEC-0,1C,
isoform PLEC-0,1C,2A,3A and isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soform PLEC-1D
                                                                                                                                                                                                            'FTId=VSP
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                                                                                                                                                                                                                                                                                                                                                                                                     2A)
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                                                                                                                                                                                                                                                                                                      (in isoform PLEC-11)
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                                                                                                                                                                                                                         (in isoform
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70;
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                                                                                                           Length 964;
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                                                 Coiled coil; Repeat; Structural protein;
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Cytoskeleton; Actin-binding;

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16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
15-OCT-2001 (Rel. 43, I
15-MAR-2004 (Rel. 43, I
Plectin 1 (PLTN) (PCN)
protein) (IFAP300) (Fra
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malecz N., Foisner R., Stadler C., Wiche G., "Identification of plectin as a substrate of p34cdc2 kinase mapping of a single phosphorylation site."; J. Biol. Chem. 271:8203-8208(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
SMART; SM00033; CH; 2.

SMART; SM00250; PLEC; 34.

PROSITE; PS00019; ACTININ 1;

PROSITE; PS00020; ACTININ 2;

PROSITE; PS50021; CH; 2.
                                                                                                                InterPro; IPR001715; Calponin-like.
InterPro; IPR001101; Plectin repeat.
InterPro; IPR002107; Spectrin.
Pfam; PF00307; CH; 2.
Pfam; PF00681; Plectin; 20.
                                                                                                                                                                                                                  InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hammater plectin ortholog.";
Piochem. Biophys. Res. Commun. 273:183-187(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldman R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20334248; PubMec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enkaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The 300-kDa intermediate filament-associated
                                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 actin-binding domain.
SIMILARITY: Contains 2 calponin-homology (CH) domains.
SIMILARITY: Contains 32 plectin repeats.
SIMILARITY: Contains 4 spectrin repeats.
SIMILARITY: Belongs to the plakin or cytolinker family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                also in the regulation of their dynamics.
SUBUNIT: Homodimer or homotetramer.
DOMAIN: The N-terminus interacts with actin, the C-t vimentin, desmin, GFAP, cytokeratins, lamin B; where and the C-terminus can bind integrin beta-4.
PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION INTERMEDIATE FILAMENTS DURING MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Interlinks intermediate filaments with microtubules and microfilaments and anchors intermediate filaments to desmosomes of hemidesmosomes. May be involved not only in the crosslinking and stabilization of cytoskeletal intermediate filaments network, but
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; Chordata; Craniata; Vertebrata; Euteleostomi;
; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Q9wtv1 rattus norv
Q17840 caenorhabdi
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Q86ri6 plasmodium	Q86rk4 plasmodium	N.	Q98pc6 rhizobium l				P91731 hyphantria		o.		Q9k756 bacillus ha	ibrio sp.	007088 bacillus th	Q7x2h0 streptomyce	Q9w2m7 drosophila	Q8iva4 homo sapien	Q96hi7 homo sapien	8	♂	015792 plasmodium		Q8ibz6 plasmodium	015791 plasmodium	Q8yal3 listeria mo		synechocy		

# ALIGNMENTS

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                                                                                 Dermatchphagoides farinae.";

RI Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

BMBL; AF178772; AAD52672.1; -

RGO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:00016798; F:chitin binding; IEA.

GO; GO:00016798; F:chitin binding; IEA.

RGO; GO:0005575; F:carbohydrate metabolism; IEA.

RGO; GO:0005575; F:carbohydrate metabolism; IEA.

RGO; GO:0005575; Chitin metabolism; IEA.

RGO; GO:0006030; F:chitin bind perA.

InterPro; IFR001257; Chitin bind perA.

InterPro; IFR001257; Chitin bind perA.

InterPro; IFR001257; Glyco_hydro_18.

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R InterPro; IFR001579; Glyco_hydro_18; 1.

R ProDom; PD000471; Glyco_hydro_18; 1.

R PROSITE; SM00494; ChtBD2; 1.

R SMART; SM00636; Glyco_18; 1.
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98kDa HDM allergen.
Dermatophagoides farinae (House-dust mite).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Eukaryota; Metazoa; Arthropoda; Chelicerata; Psoroptidia; Analgoidea;
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Pyroglyphidae; Dermatophagoides.
NCBI_TaxID=6954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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100.0%; Score 64; DB 5; 100.0%; Pred. No. 0.0025; tive 0; Mismatches 0;
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GO; GO:0008061; F:chitin binding; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016975; F:carbohydrate metabolism; IEA.
InterPro; IPR001223; Glyco, hydro, 18.
InterPro; IPR001223; Glyco, hydro, 18.
InterPro; IPR00123; Glyco, hydro, 18.
InterPro; IPR0012579; Glyco, hydro, 18.
InterPro; IPR001579; Glyco, hydro, 18; 1.
Pfam; PF00704; Glyco, hydro, 18; 1.
Pfam; PF00704; Glyco, hydro, 18; 1.
Pfam; PF01476; Lysm, 4.
PF0Dom; PD000471; Glyco, hydro, 18; 1.
SMART; SM00257; ChtBD1; 2.
SMART; SM00257; Lysm, 5.
SMART; SM00257; Lysm, 5.
PROSITE; PS01095; CHITINASE, 18; 1.
PROSITE; PS01095; CHITINASE, 18; 1.
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01-FEB-1997
01-OCT-2003
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Q94298;
  Q8RHG1;
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Graves T., Wohldmann P.;
"The sequence of C. elega
Submitted (OCT-1996) to 1
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Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U70888; AAB09177.1; -.
PIR; T29275; T29275.
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STRAIN=Bristol N2;
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STRAIN=Bristol N2;
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Rhabditidae; Peloderinae;
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8; Conserv
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1484 AA;
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EMBL/GenBank/DDBJ databases.
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J. Bacteriol. 184:2005-2018(2002).
EMBL; ABG10511; AAL194159.1; -
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
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01-JUN-2002
01-JUN-2002
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01-MAR-2003
01-MAR-2003
                                                                                                                                                                                InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18; 1.
ProDom; PD000471; Glyco hydro 18; 1.
SMART; SM00636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
SEQUENCE 431 AA; 47238 MW; 929439397B9BC923 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
Kapatral V., Anderson I., Ivanova
                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning of a cDNA encoding the chit Araneus ventricosus.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ EMBL; AY120879; AAN39100.1;
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0005975; P:carbbhydrate metabolism; IEA.
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NCBI_TaxID=182803;
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Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
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                                            DKONYLALVRELK 13
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Pred. No. 2
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Q8MY79;
01-OCT-2002
01-OCT-2002
01-OCT-2003
                                                                                                                                                                                                                                                                               Pfam; PF01607; CBM 14; 1.

Pfam; PF00704; G1yco hydro 18; 2.

PfcDom; PD000471; G1yco hydro 18; 2.

SMART; SM00494; ChtBDz 1.

SMART; SM00636; G1yco 18; 2.

PROSITE; PS01095; CHITINASE 18; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB074977; BAC06447.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:000877; F:hydrolase activity; IEA.
GO; GO:0005975; P:carbobydrate metabolism; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
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Viruses; dsDNA viruses, no RNA
NCBI TaxID=170617;
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characterization of a Haemaphysalis longicornis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Haemaphysalis.
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"The complete sequence of the Adoxophyes orana Virology 311:350-365(2003).
EMBL; AF547984; AAP886559.1; -.
SEQUENCE 176 AA; 21065 MW; 73E2F36E0ED69440
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DKKNFVELVRELR
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                                                                                                                                                                                                                                                           929 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.3%;
                                                                                                                                                                                                                                                           104423 MW;
                                                                                                                                                       70.3%;
187
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Last sequence update)
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Last sequence update)
Last annotation updat
                                                                                                                               4.
                                                                                                                                                             Score 45; DB
Pred. No. 16;
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                                                                                                                               Mismatches
                                                                                                                                                                                                                                                           3D70C956DC1D93C6 CRC64;
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                                                                                                                                                                                        Length 929;
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Best Local S
Matches 7
YSEQUENCE FACUS N.A.

A Tan S.H., Degman B.M., Lehnert S.A.;

A Tan S.H., Degman B.M., Iehnert S.A.;

I "The Penaeus monodon chitinase I gene is differentially exp.

I the hepatopancreas during the moult cycle.";

I Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0005976; F:chitin binding; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0006030; P:chitin bind perA.

InterPro; IPR001223; Glyco_hydro_18.

InterPro; IPR001223; Glyco_hydro_18AS.
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Science 282:2012-2018(1998).
Science 2770035; CAA93863.1; -.
REMBL; Z70035; CAA93863.1; -.
PIR; T24074; T24074.
R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0018152; F:metabolism; IEA.
R GO; GO:008152; F:metabolism; IEA.
R GO; GO:008152; Glyco_hydro_18.
R InterPro; IPR001223; Glyco_hydro_18.
R FAEM; PF00704; Glyco_hydro_18; 1.
R PRODOM; PD000471; Glyco_hydro] 18; 2.
SMART; SM00636; Glyco_18; 1.
SEQUENCE 435 AA; 50487 MW; BFF171549CB1C952 CRC64;
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Q21859;
01-NOV-1996
01-NOV-1996
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9Y0D4;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Cru
Bumalacostraca; Eucarida; Decapoda;
Penaeidae; Penaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matthews
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Tan S.H., Degnan B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penaeus monodon (Penoeid shrimp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the nematode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oda; Chromadorea;
Caenorhabditis.
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Pred. No. 11;
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oda; Dendrobranchiata; Penaecidea;
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Best Local S
Matches 7
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF062038; AAD22610.1; -.
HSSP; P07254; ICTN.
G0; G0:0016787; F:hydrolase activity; II
G0; G0:00016787; F:hydrolase activity; II
G0; G0:0008152; P:metabolism; IEA.
InterPro; IPR001223; Glyco hydro 18.
Pfam; PF00704; Glyco hydro 18; 1.
ProDom; PD000471; Glyco hydro 18; 1.
SMART; SM00636; Glyco 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01607; CBM 14; 1.
Pfam; PF00704; Glyco hydro 18; 1.
PrODom; PD000471; Glyco hydro 18; 1.
SMART; SM00494; ChtBD2; 1.
SMART; SM00636; Glyco 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
Glycosidase; Hydrolase.
                                                                                                                                                                           Q17840;
Q17840;
01-NOV-1996;
01-NOV-1996;
01-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wendling U., Boots A.M.H., van Eden W.; "Cloning of the rat homologue of Human Cartilage glycopr potential autoantigen in arthritis."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Lewis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein-39 (Fragment).
                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                        C08H9.14 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                        C08H9.14
                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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  FROM N.A
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352 AA;
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                            Nematoda;
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                                                                   oda; Chromadorea;
Caenorhabditis.
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Last annotation updat
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Last sequence update)
Last annotation update)
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Pred. No. 21;
4; Mismatches
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Pred. No. 24;
3; Mismatches
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                                                                                        Rhabditida; Rhabditoidea;
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; Murinae; Rat'
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Best Local :
                                                        Matches
                                                                             Query Match
Best Local (
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G0; G0:0016787; F:hydrolase activity; I;
G0; G0:0008152; P:metabolism; IEA.
InterPro; IPR001223; Glyco_hydro_18.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 2.
SMART; SM00636; Glyco_18; 1.
SEQUENCE 399 AA; 45871 MW; 9E99EF2E
                                                                                                                                                  WormPep; C08H9.12; CE02997.
GO; GO:0016787; F:hydrolase activity; I;
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001223; Glyco_hydro_18.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PF000471; Glyco_hydro_18; 2.
SMART; SM00636; Glyco_18; 1.
SEQUENCE 460 AA; 52809 MW; 6984C059;
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Submitted
[2]
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Q17836;
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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EMBL; Z54342; CAA91153.1; -.
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01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                EMBL; Z54342; CAA91149.1; -. PIR; T19111; T19111.
                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode investigating biology."; science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .nvestigating
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                                                     Similarity 7; Conserv
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DKONYLALVRELK 13
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                                                  Score 42; DB
Pred. No. 27;
3; Mismatches
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Last annotation update)
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Pred. No.
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolthakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Deventor I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Deventor I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Deventor I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Deventor I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Deventor I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodson K., Doug L.E., Downes M., Deng Z., Mays A.D., Dew II., Dickova B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Glasrt W.M., Glasser K.,
RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Zhong W., Zhong W., Shong H., Wang A.H., Wang X.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Cheng S., Ra, Wyers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
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Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dreenek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Tyler D.,

A Milliams S.M., Strong R., Svirskas R., Tector C., Tyler D.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

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Q9W2M6; Q8SYH
Q1-MAY-2000
Q1-QCT-2002
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Eukaryota; Metazoa; Arthropoda; Hasoda; Insecta; Pterygo
Neoptera; Endopterygota; Olptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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CHT4 OR CG3986.
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01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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G0; G0:0005576; C:extracellular; IEA.
G0; G0:0008061; F:chitin binding; IEA.
G0; G0:0016798; F:hydrolase activity, acting on gl
G0; G0:0016798; F:hydrolase activity, acting on gl
G0; G0:0005975; P:carbohydrate metabolism; IEA.
G0; G0:0006030; P:chitin metabolism; IEA.
InterPro; IPR001257; Chitin bind PerA.
InterPro; IPR00123; Glyco_hydro_18AS.
InterPro; IPR001579; Glyco_hydro_18AS.
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Miranda S., Phouanenavong
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Adams M.D., Celniker
Submitted (MAR-2000)
SEQUENCE FROM N.A. Lloyd C.R.;
                                                               NCBI_TaxID=6239;
                                                                                             Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
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er S.E.,
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PIR; T28113; T28113.

WormPep; ZK938.6; CE02400.

Wo Co.0016787; F:hydrolase activity; IE
GO; GO:0018152; P:metabolism; IEA.

InterPro; IPR001223; Glyco_hydro_18.

Pfam; PF000704; Glyco_hydro_18; 2.

ProDom; PD000471; Glyco_hydro_18; 3.

SMART; SM00636; Glyco_18; 1.

SEQUENCE 522 AA; 60207 MW; 38646848!
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GO; GO:0016787; F:hydrolase activity; II
GO; GO:0008152; F:hydrolase activity; II
GO; GO:0008152; F:metabolism; IEA.
InterPro; IPR001223; Glyco_hydro_18; 1.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 2.
SMART; SM0636; Glyco_hydro_18; 2.
SMART; SM0636; Glyco_18; 1.
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Q23675; PRELIMINARY;
Q1-NOV-1996 (TrEMBLrel. 01,
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
science 282:2012-2018(1998).
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Science 282:2012-2018(1998).
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DENNYLMFIRELR 303
                                                DKONYLALVRELK 13
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                                                                                            Conservative
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Search completed: March Job time: 4.6159 secs

22,

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06:59:20

RESULT 15

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                                                             Query Match
Best Local (
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GO; GO:0008061; R:chitin binding; IEA.
GO; GO:0016798; F:bydrolase activity, acting on gl
GO; GO:0016798; F:bydrolase activity, acting on gl
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001002; Chitin binding 1.
InterPro; IPR001223; Glyco_hydro_18AS.
InterPro; IPR001579; Glyco_hydro_18AS.
Pfam; PP00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00270; ChiBD1; 3.
SMART; SM00266; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; 1.
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Q22468 (TYEN
01-NOV-1996 (TYEN
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01-OCT-2003 (TYEN
T13H5.3 protein.
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EMBL; Z66524; CAA91419.1; -.

PIR; T24898; T24898.

HSSP; P27275; LVMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                Glycosidase; Hydrolase.
SECHENCE 633 AA; 70746 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               Lightning J.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                 'Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    nvestigating biology.
                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                             Local Similarity
164 DRRNYVNLMRELR 176
                       DKONYLALVRELK 13
                                                  Conservative
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53.88;
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                                                             Score 42; DB 5;
Pred. No. 38;
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Maximum Match 100%
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64
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1: geneseqp1980s:*
2: geneseqp1990s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	თ	ហ	4.	ω	2	Д	No.	Result
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45	44	43	42	41	40	39	38	37	36	ι. U	34	33	32	31	30	29	28	27	26
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ABG27548	AAU30929	AAU32370	ABG08690	ABG12547	ABB58615	ABP72626	ABG05422	ABG05413	ABG06842	ABB65118	AAB58662	AAY52901	AAY68247	ABG05403	ABG03849	ABG14887	ABG14423	ABG05109	ABB64366
Abg27548	Aau30929	Aau32370	Abg08690	Abg12547	Abb58615	Abp72626	Abg05422	Abg05413	Abg06842	Abb65118	Aab58662	Aay52901	Aay68247	Abg05403	Abg03849	Abg14887	Abg14423	Abg05109	Abb64366
Nove	Nove	Nove	Nove.		Drosophil		Novel	Novel	-	Drosophil		Murine	Murine	Novel	Novel	Novel	Novel	Novel	Drosophi

# ALIGNMENTS

# AAY52516 standard; peptide; 13 AA.

AAY52516;

22-FEB-2000

(first entry)

House dust mite allergen protein (map) A/B fragment map(6).

Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.

Dermatophagoides farinae.

WO9954349-A2

28-OCT-1999.

17-APR-1998; 13-MAY-1998; 02-SEP-1998; 16-APR-1999; 98US-00062013. 98US-0085295P. 98US-0098909P. 99WO-US008524.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber

WPI; 2000-052700/04.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Claim 3; Page 69; 154pp; English.

RRSULT 1
AAV552516
ID AAV5
XX AAV5
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XX Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWM -map) composition. The HWW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. The HWW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines,

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Similarity

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RESULT 2
AAU96320
ID AAU9
The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-protein acceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A composition is useful for desensitioning a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-per HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (19) or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to 19E, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
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Matches
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                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 70; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                         New mite allergenic protein isolated from Dermatophagoides, design
Der HMW-map protein, useful as a vaccine for treating mite allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2001; 2001WO-US028730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000; 2000US-00662293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mite allergenic protein; immunocomplex formation.
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RESULT 3
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                                   This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf99-536, the mature form of pDerf98-555 (AAYS2523). PDerf98-536 CC has a molecular weight of 98 kD, comprising 536 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite component of the Dermatophagoides farinae high molecular weight mite component of the Dermatophagoides farinae high molecular weight mite component of the Dermatophagoides farinae high molecular weight mite component of the presence of proteins that bound to Igz present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, capitaes, canimals, equines, humans, other pets, and work or compositions to a skin test. The proteins and peptides can also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to they can be used as vaccines to passively immunise animals against dust conclude mater and as tools to composition to the proteins and peptides can also be used to chapter a perfect of potential uses. For example, they can be used as vaccines to passively immunise animals against dust conclude mater and peptides can also be used to composition to mite hypersensitivity, as positive controls in test kits and as tools to conclude mater and as tools to conclude material materi
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Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY52525 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mite allergen protein; map; high molecular weight; HMW-map; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     House dust mite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY52525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 125-127; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ38579, AAZ38580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HESK-) HESKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-052700/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKONYLALVRELK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00062013.
98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (D. farinae) mite allergen protein (map)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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; Mismatches
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDerf98-536
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Matches Query Match

Local

Similarity

100.0%;

Score 64; Pred. No.

DB 3; 0

Length 536;

Conservative

0

Mismatches

Indels

0

Gaps

0

Sequence

536 AA;

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AAU96329
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RESULT 5
AAY52523
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AC AAY5
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Best Local
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DMA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting between the contract of the contract of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                              AAY52523;
                                                                                     AAY52523 standard; protein; 555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 125-127; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mite allergenic protein isolated from Dermatophagoides, designa
Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-351888/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2001; 2001WO-US028730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Der HMW-map polypeptide #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU96329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2002
                                                                                                                                                                                                                                      153
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                                                                                                                                                                                                                                                                                                                                                       l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK69575
                                                                                                                                                                                                                                      DKONYLALVRELK 165
                                                                                                                                                                                                                                                                                          DKONYLALVRELK 13
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                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 64; DB 5; ilarity 100.0%; Pred. No. 0.0057; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 536;
                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 6
AAU96327
ID AAU9
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AAU96327

standard; protein;

555 AA

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                                                                                                                         This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD, compositiong 555 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) composition. The HWM-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to 1gB present in mite-allergic dog encoding them, may be used in therappeutic compositions to modify an animals hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as allergens from a mixture of proteins
                                                            Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                      Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 111-113; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; maph; mapb; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HESK-) HESKA CORP.
 172
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                              ட
DKONYLALVRELK 184
                            DKONYLALVRELK 13
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                                                         100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Mature PDerf98-555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Signal peptide"
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555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weber
                                                            0
                                                         Score 64; DB 3;
Pred. No. 0.0059;
Mismatches 0
                                                                                      Length 555;
                                                           Indels
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                                                         Gaps
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AAU96328
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DT 15-J
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DE Der
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Best Local
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                                                                                                                                                                                AAU96328 standard; protein; 555 AA
                                                            Der HMW-map;
                                                                                         Der HMW-map polypeptide #15.
                                                                                                                          15-JUL-2002
                                                                                                                                                          AAU96328;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated mite allergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 114-116; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-351888/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
                                                 mite allergenic
                                                                                                                                                                                                                                                                                                                                                                                                                    represent Der HMW-map polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-2001; 2001WO-US028730
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                               immunocomplex formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mite allergenic protein isolated from Dermatophagoides, HMW-map protein, useful as a vaccine for treating mite \hat{\epsilon}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMW-map polypeptide #14
                                                                                                                                                                                                                                                                172
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                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                            DKONYLALVRELK 13
                                                                                                                                                                                                                                                                DKONYLALVRELK 184
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                                                                                                                                                                                                                                                                                                                           Conservative
                                          American house dust mite; antiallergic; mite; I nic protein; immunoglobulin E; hypersensitivity;
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                         Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                   DB 5; L., 0.0059; 0;
                                                                                                                                                                                                                                                                                                                                                    Length 555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein of
d its related nucleic
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RESULT 8
AAY52535
ID AAY5
XX AAY5
AC AAY5
XX O6-A
DT 06-A
DT 22-F
XX Mite
KW hype
KW hype
KW hype
KW hype
KW cani
XX Dern
XX Dern
XX Mod:
FT Mod:
FT Mod:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dermatophagoides, designated Der HMW-map proteil, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (19) sor Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgB, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AA096314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local (
                                                                                                                                            Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                     06-AUG-2003
22-FEB-2000
                                                                                                                                                                                                                                                                                                                       AAY52535;
                                                                                                                 Dermatophagoides pteronyssinus
                                                                                                                                                                                                                                D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490
                                                                                                                                                                                                                                                                                                                                                     AAY52535 standard; protein; 490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mite allergenic protein isolated from Dermatophagoides, designa
Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated mite allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 120-122; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-351888/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                            172 DKQNYLALVRELK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DKONYLALVRELK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                115. .117
                                                                              Location/Qualifiers
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Pred. No. 0.0059;
Pred. No. 0.0059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 555;
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Modified-site

note=

"Asn is N-glycosylated" "Asn is N-glycosylated"

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RESULT 9
AAU96339
ID AAU9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-490, the mature form of pDerp98-599. PDerp98-490 chas a molecular weight of 98 kD, comprising 490 amino acids, and has a chigh degree of homology with the D. farinae mature 98 kD allergen, maps (AAY52525). Nucleic acid molecules encoding poerp98-490 were isolated from a D. pteronyssius cDNA library by hybridisation with a probe encoding the D. farinae high molecular weight map (HMW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, compositions to modify an animal's compositions to modify an animal's compositions to modify an animal of them, compositions to modify an animal of them, compositions to modify an animal of the proteins and birds, especially felines, canines, equines, humans, conther pets, and work or domestic animals. The proteins and content pets, and work or domestic animals. The proteins and content pets, and work or domestic animals. The proteins and content pets, and the content pets and birds, especially felines, which have a variety of potential uses. For example, they can be used as vaccines to passively contential uses. For example, they can be used as vaccines to passively
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Best Local
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                                                                                                                                                        Der HMW-map; American house dust mite; antiallergic; mite allergenic protein; immunoglobulin E; hypersensi
                                                                                                                                                                                                             Der HMW-map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 147-149; 154pp; English
                                                                                                                                                                                                                                                  15-JUL-2002
                                                                                                                                                                                                                                                                                                                 AAU96339 standard; protein; 490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 490 AA;
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02-SEP-1998;
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 14-SEP-2001; 2001WO-US028730.
                                     21-MAR-2002
                                                                       WO200222807-A2
                                                                                                        Dermatophagoides
                                                                                                                                            immunocomplex formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a nixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                           153
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hunter SW,
                                                                                                                                                                                                             polypeptide #26.
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                                                                                                                                                                                                                                               (first entry)
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98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB
Pred. No. 0.02
0; Mismatches
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0.028;
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RESULT 10
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                           Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB;
                                                                                                                                                                                                                                                                                                                                   06-AUG-2003
22-FEB-2000
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                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                       D. pteronyssius 98 kD mite allergen protein (map)
                                                                                                                                                                                                                                                                                                                                                                                                          AAY52533 standard; protein;
                                                                                      WO9954349-A2
                                                                                                                                                         Peptide
                                                                                                                                                                                                    Dermatophagoides pteronyssinus.
                                                                                                                                                                                                                                              hypersensitivity reaction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mite allergenic protein isolated from Dermatophagoides, designa HMW-map protein, useful as a vaccine for treating mite allergy.
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DB; ABK69585.
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12; Conserv
                                                                                                                                                                                                                               veterinary; antibody;
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(first entry)
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                                                                                                                                                                      Location/Qualifiers
                                                                                                                                            note= "Signal peptide"
                                                                                                                                .509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.8%;
                                                                                                               "Mature PDerp98-509"
                                                                                                                                                                                                                              therapy; treatment;
dy; vaccine; immunis;
                                                                                                                                                                                                                                                                                                                                                                                                          509
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Pred. No. 0.028;
0; Mismatches
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                                                                                                                                                                                                                                              diagnosis; human; feline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 490;
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17-APR-1998;

98US-00062013. 99WO-US008524

16-APR-1999;

28-OCT-1999

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RESULT 11
AAU96337
ID AAU96
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AC AAU96
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DET H
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DET H
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AC
DET
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Der HMW-map; American house dust mite; antiallergic; mite allergenic protein; immunoglobulin E; hypersens: immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Der HMW-map polypeptide #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU96337 standard; protein; 509 AA.
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02-SEP-1998;
                                  Mccall CA,
                                                                                                                                                           14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                    14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                                                                                                                                                               WO200222807-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2002 (first entry)
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                                                                                                  (HESK-) HESKA CORP
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                                      Hunter SW,
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98US-0098909P.
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                                      Weber ER
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Pred. No. 0.02!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-351888/38.
N-PSDB; ABK69581.
                                                                                                                                        WFI; 2002-351888/38.
N-PSDB; ABK69583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dermatophagoides, designated Der HMM-map protein, and its related nucleic acid. The Der HMM-map protein is useful for eliciting an immune response against Der HMM-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                    New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                             Mccall CA,
                                                                                                                                                                                                                                                                     14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mite allergenic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Der HMW-map; American house dust mite; antiallergic; mite; IgB; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Der HMW-map polypeptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                           21-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                              WO200222807-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Dermatophagoides farinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                               immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU96338;
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                                                                                                                                                                                                                                  (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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Pred. No. 0.029;
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic

Claim 12; Page 139-141; 161pp; English.

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Matches 12
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                                                                                                                                                                                 Tick chitinase and its encoded polynucleotide, applicable in develor diagnostics, agents for exterminating mite, remedies or preventives mite mediated-infections e.g. piroplasmosis and Q fever.
                                                                                                                                                                                                                                                                                        Fujisaki K, Nagasawa
Yu M, Tsuji N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chitinase; antiinflammatory; virucide; antipyretic; tick; mite; piroplasmosis; Q fever; viral encephalitis; vaccine.
                                                                                                                                                                                                                                              N-PSDB; ADB78971.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemaphysalis longicornis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tick chitinase #SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB78972 standard;
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                                                                                                                                                                                                                                                                                                                                  MEIJI SEIKA KAISHA LTD
FUJISAKI K.
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The invention relates to a tick chitinase polypeptide, or its derivative that has chitinase activity. Also disclosed is a vector containing the polymucleotide, a transformant containing the polymucleotide, a process for producing the polypeptide by culturing the transformant, drugs containing the polypeptide, and a method for exterminating mites by administering an effective dose of the polypeptide. The protein and its encoded polymucleotide are applicable in developing diagnostics, agents and the polymucleotide are applicable in developing diagnostics, agents

Claim 1; Page 33-39; 47pp; Japanese.

for exterminating mites, remedies or preventives, including vaccines, for mite mediated-infections e.g. piroplasmosis, Q fever or viral encephalitis. The produced drugs are new and mostly likely less prone to

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RESULT 14
ABB49221
ABB49221
AC ABB49
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Matches
for biosynthesis and biodegradation, especially biosynthesis of vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene excepts and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, antibodies, identification of L. monocytogenes and related organisms, antibodies, identification of L. monocytogenes and related organisms.
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Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
Rose M, Voss H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes protein #1925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for Listeria monocytogenes, useful e.g. for fisteria and related bacterial infections,
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Pred. No. 30;
4; Mismatches
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The invention relates to isolated polynucleotide (I) and polypeptide (II) creation (IC) is useful as hybridisation probes, polymerase chain (I reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used (I) is useful in gene therapy techniques to restore normal (II) activity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal (II) useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food (II) supplement. (II) and (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders (I involving aberrant protein expression or biological activity. The (I is a polypeptide and polymucleotide sequences have applications in (II) are useful for treations (II) are useful for meaning (II) are useful for treations (II) are useful for meaning (II) are useful for assess biodiversity (II) are useful for assess biodiv
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                      ftp.wipo.int/pub/published_pct_sequences
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23-AUG-2000; 2000US-00649167.
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Query Match Best Local Similarity 7; 64.1%; 58.3%; Score 41; DB 4; Pred. No. 1.9e+02; 1; Indels Length 1042

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Search completed: March 22, 2004, 06:51:41 Job time: 4.95275 secs

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       Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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18, Appl
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6743, Ap
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12804, A
23404, A
45, Appl
270, Appl
19361, A
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iption  uence 7, Appli uence 21, Appl uence 15, Appl uence 18, Appl uence 14, Appl uence 35, Appl uence 38, Appl uence 38, Appl uence 38, Appl uence 3743, Appl	***  **  have a ng printed,		econds updates/sec
00 Z ·· H 39 70	RESULT 1  US-10-218-743-7  US-10-218-743-7  / Sequence 7, Application US/10218743  / Publication No. US20030096779A1  / GENERAL INFORMATION: / APPLICANT: McCall, Catherine A. / APPLICANT: Muter, Shirley Wu / APPLICANT: Weber, Eric R. / TITLE OF INVENTION: AND USES THEREOF // FILE REFERENCE: ALC-C3 // CURRENT APPLICATION NUMBER: US/10/218,743 // CURRENT FILING DATE: 2002-08-13 // PRIOR APPLICATION NUMBER: US/09/292,225 // PRIOR APPLICATION NUMBER: US/09/292,225 // PRIOR APPLICATION NUMBER: 60/098,909 // PRIOR APPLICATION NUMBER: 1999-09-02	26 36 56.2 185 12 US-10-424-599-237039 Sequence 237039, 27 36 56.2 293 13 US-09-811-007-40 Sequence 40, Appl 28 36 56.2 293 13 US-10-052-634-40 Sequence 40, Appl 30 36 56.2 293 14 US-10-052-051-40 Sequence 40, Appl 31 36 56.2 293 14 US-10-062-051-40 Sequence 40, Appl 32 36 56.2 293 14 US-10-062-920-40 Sequence 40, Appl 32 36 56.2 358 12 US-10-062-920-40 Sequence 40, Appl 33 36 56.2 358 12 US-10-424-599-273219 Sequence 273219, 35 36 56.2 361 12 US-10-424-599-273219 Sequence 273219, 36 56.2 361 12 US-10-001-835-189 Sequence 273219, 37 36 56.2 1031 14 US-10-002-56A-153 Sequence 273219, 38 36 56.2 1031 14 US-10-002-56A-153 Sequence 273219, 39 36 56.2 1272 12 US-10-014-270-30 Sequence 2757, Appl 39 36 56.2 1275 14 US-10-025-201-3 Sequence 30, Appl 41 35 54.7 152 14 US-10-025-201-3 Sequence 30, Appl 42 35 54.7 195 9 US-09-764-846-199 Sequence 75, Appl 44 35 54.7 195 14 US-10-091-483-199 Sequence 799, Appl 54.7 195 14 US-10-091-483-199 Sequence 199, Appl 54.7 218 15 US-10-314-434-182 Sequence 199, Appl 54.7 218 15 US-10-314-434-182 Sequence 199, Appl 54.7 218 15 US-10-344-599-251698 Sequence 251698, Appl 54.7 244 12 US-10-424-599-251698	39 60.9 407 15 US-10-369-493-20271 Sequence 38 59.4 987 14 US-10-156-761-14515 Sequence 37 57.8 331 14 US-10-128-714-8255 Sequence 37 57.8 407 12 US-10-282-122A-65624 Sequence 37 57.8 513 15 US-10-369-493-21317 Sequence 37 57.8 1097 14 US-10-369-493-5525 Sequence 37 57.8 1097 14 US-10-369-493-5525 Sequence 37 57.8 1097 14 US-10-369-493-5720 Sequence 37 57.8 1097 14 US-10-369-493-18943 Sequence 38 56.2 183 15 US-10-369-493-20260 Sequence 38 56.2 184 15 US-10-369-493-20260 Sequence

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Query Match Best Local S Matches 13

ch 100.0%; Score 64; DB 14; l Similarity 100.0%; Pred. No. 6.9e-05; 13; Conservative 0; Mismatches 0;

Length 13; Indels

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; ORGANISM: Dermatophagoides farinae
US-10-218-743-15
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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SEQ ID NO 21
SEQTH: 536
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Sequence 15, Application US/10218743
Publication No. US20030096779A1
                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REPERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 536
TYPE: PRT
ORGANISM: Dermatophagoides farinae
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                                                                                                                                                                                                                                                                                                                                                                                                                               URRENT APPLICATION NUMBER: US/10/218,743
URRENT FILING DATE: 2002-08-13
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                                                  LENGTH: 555
TYPE: PRT
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                                                                                                                                              ID NOS: 49
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Pred. No. 0.0042;
); Mismatches 0;
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APPLICANT: HUNTER, STAIRLEY WU
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: 00/098,909
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR PRILING DATE: 1998-09-02
PRIOR PRILING DATE: 1998-09-03
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR APPLICATION NUMBER: 60/098,565

PRIOR APPLICATION NUMBER: 09/062,013 PRIOR FILING DATE: 1998-04-17

Sequence 41, Application US/10218743
Publication No. US20030096779A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.

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                                                                                                                                                                                ; ORGANISM: Dermatophagoides farinae
US-10-218-743-18
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PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Publication No. US20030096779A1
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Best Local 9
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF PILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 49
                                                                                                           Local
172 DKONYLALVRELK 184
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                                           1 ркомунацияных 13
                                                                                         l Similarity
13; Conserv
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Similarity 100.0%;
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                                                                                                         100.0%; Score 64;
100.0%; Pred. No.
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Pred. No.
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US-10-218-743-38
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TYPE: PAT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-35
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TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-41
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Publication No. US20030096779A1
GENERAL INFORMATION:
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SEQ ID NO 41
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Best Local Similarity
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
                                                                                          APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APELICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
FRIOR APPLICATION NUMBER: US/09/292,225
FRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
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PRIOR FILING DATE: 1998-04-17
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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OR FILING DATE: 1998-09-02
OR APPLICATION NUMBER: 60/085,295
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/098,565
OR FILING DATE: 1998-04-17
OR FILING DATE: 1998-04-17
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Pred. No. 0.021;
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US-10-424-599-172346

GENERAL INFORMATION:

NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 172346

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)|B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

Sequence 172346, Application US/10424599 Publication No. US20040031072A1

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Query Match
Best Local Similarity
Tatches 9; Conserve
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US-10-369-493-6743
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                                                                                                                                                                                                          SEQ ID NO 6743
LENGTH: 617
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SEQ ID NO 38
LENGTH: 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6743, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                              APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatter, Steven C.
APPLICANT: Slatter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE REFERENCE: 38-10(52052)B
CURRENT FILLNG DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493
CURRENT FILLNG DATE: 2003-02-8
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-91
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/085,295 PRIOR FILING DATE: 1998-05-13
                                                                                                                                                                     ORGANISM: Caenorhabditis elegans
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Local Similarity 92.3%;
186 DMANYVALVKELK 198
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                                     1 DKQNYLALVRELK 13
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                                                                                          71.9%;
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Pred. No. 0.02
0; Mismatches
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                                                                                        Pred. No. 8.
                                                                      Mismatches
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Sequence 12.

Sequence 12.

Publication No. 12.

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

PUBLICANT: Slater, Steven C.

PUBLICANT: Goldman, Barry S.

PUBLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_126645C.1.pep
US-10-424-599-172346
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COTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12804
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US-10-369-493-12804
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12804
LENGTH: 789
                                                                                                                                                                                                                                                                                                                                                Sequence 23404, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23404
LENGTH: 84
TYPE: PRT
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Publication No. US20030233675A1
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                                                                                                                            CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                    APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                    PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Glycine FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Aspergillus nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 58.3%; Local Similarity 58.3%; hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 69.7 hes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 DYENYVSLVREM 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DKONYLALVRELK 13
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Pred. No. 6.4;
2; Mismatches
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Pred. No. 89;
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR PFILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR APPLICATION NUMBER: 60/35,149
PRIOR APPLICATION NUMBER: 60/35,149
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/374,967
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/315,102
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
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                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-097-340-45
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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TYPE: PRT
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                                                                                               Local
146 DKQHFTTLIKEMK 158
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                                   1 DKONYLALVRELK 13
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                                                                            h 62.5%;
Similarity 46.2%;
6; Conservative
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Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
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Karen GLATT
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Shubhangi KAMATKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gordon B. MILLS
Robert C. BAST, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Karen LU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ami SEN
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Pred. No.
                                                                                               Score 40; DB
Pred. No. 60;
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                                                                                                                      DB 14; Length 383;
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RESULT 13 US-10-295-027-270

Sequence 270, Application US/10295027 Publication No. US20030232350A1

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; Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1386; SOFTWARE: PatentIN Ver. 2.1; SEQ ID NO 270; LENGTH: 383; TYPE: PRT ROADNISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/295,027

CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: US 09/663,733

PRIOR FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13

PRIOR PPLICATION NUMBER: US 60/335,394

PRIOR APPLICATION NUMBER: US 60/335,394

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR FILING DATE: 2001-11-21
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                                                                                                                                                                                                                                                                                                                                              Sequence 19361, Application US/10369493 bublication No. US20030233675A1
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                     APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
                                                                       CURRENT APPLICATION NUMBER: US/10/369,493
                                                                                                                                                                                                                                                                                              APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/340,376 FILING DATE: 2001-12-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/347,349 FILING DATE: 2002-01-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKQHFTTLIKEMK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKONYLALVRELK 13
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Hevezi, Peter A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB Pred. No. 60; 5; Mismatches

    See File Wrapper or PALM

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 383;
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; TYPE: PRT; ORGANISM: Myxococcus xanthus US-10-369-493-19361
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US-10-369-493-16746
Search completed: March 22, 2004, 07:45:49 Job time: 3.65926 secs
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                                                                                                                                                                                              US-10-369-493-16746
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16746
LENGTH: 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16746, Application US/10369493 Publication No. US20030233675A1
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                                                                                                                               Best Local Similarity Matches 7; Conserv
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EXERESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
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                                                                                                                                                                                                             TYPE: PRT ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 392
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                                                               225 DKONFTLLLQELR 237
                                                                                               1 DKONYLALVRELK 13
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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                                                                                                                               Conservative
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53.8%;
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53.8%;
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Pred. No. 1.1e+02;
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Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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length: 2000000000
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Gapop 10.0 , Gapext 0.5
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64
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Maximum Match 100%
Listing first 45 summaries
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   DKQNYLALVRELK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                  Length
   Search time 1.0478 Seconds (without alignments)
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                                                                                                                  Sequence 2, Appli
Sequence 16, Appl
Sequence 21, Appl
                                                                                                                                                            Sequence 7, Appli
Sequence 21, Appl
Sequence 15, Appl
Sequence 18, Appl
Sequence 41, Appl
Sequence 35, Appl
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Sequence
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                                                                                          79, Appl
79, Appl
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2, Appl
4, 4866, Ap
4, 4356, Ap
                                                                    Appl
Appl
Appl
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Sequence 21, Application US/09292225

Patent No. 6455686

GENERAL INFORMATION:

APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Heber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUC
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3

TITLE OF ADDITION NUMBER: US/09/292,225

NUCLEIC

ACID MOLECULES,

PROTEINS

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1 DKONYLALVRELK 13 1 DKONYLALVRELK 13 Conservative

US-09-292-225-21 RESULT 2 Ś

Query Match
Best Local Similarity
Matches 13; Conserv

100.0%;

Score 64; Pred. No. Mismatches

4e-05; DB

4.

Length 13;

Indels

0

Gaps

0

0;

; LENGTH: 13 ; TYPE: PRT ; ORGANIZM: Dermatophagoides farinae US-09-292-225-7

TITLE OF FILE REFE CURRENT E CURRENT E EARLIER E EARLIER F EARLIER F EARLIER F EARLIER R EARLIER R EARLIER R EARLIER R EARLIER R EARLIER OF SOFTWARE SEQ ID NO LENGTH:	RESULT 1 US-09-292-225. Sequence 7, Patent No. GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:		4 4 4 5 4 3	42	4.0	υ ω ( ) & -	36	υ A.R	u u v	3 1 1 1	30	2 2 8 0	
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INVENTION: NOV. INVENTION: AND RENCE: AL-2-C3 PPLICATION NUM ILING DATE: 19 PPLICATION NUM ILING			54.7 54.7	44		42.4	4.4	54.7	54.7	4.		54.7	I
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HEREOF 109/292,225 5 1098,909 2 1085,295 1098,565 1062,013 1062,013		ALIGNMENTS	US-09-134-001C-5254 US-09-134-001C-3524 US-09-543-681A-4337	08-370-476-6	US-08-481-985B-66	US-08-370-476-72	US-08-484-905-72	481-985B- 370-476-7	US-09-314-701-14 US-08-484-905-77	09-314-701-	-08-370-476-80	US-08-484-905-80 US-08-481-985B-80	
ACID MORECUES			Sequence Sequence Sequence	Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	•
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RESULT 4
US-09-292-225-18
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ 1D NOS: 49
SOFTWARE: Patentin Ver: 2.0
Sequence 18, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
APPLICANT: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-09-292-225-15
Sequence 15, Application US/09292225
Patent No. 6455686
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SEQ ID NO 15

LENGTH: 555

TYPE: PRT

ORGANISM: Dermatophagoides farinae
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LENGTH: 536
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EARLIER
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EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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les 13; Conserv
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APPLICATION NUMBER: 60/098,909
FILING DATE: 1998-09-02
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RESULT 5
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FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/08,909
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/08,565
EARLIER APPLICATION NUMBER: 60/08,565
EARLIER APPLICATION NUMBER: 60/08,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
NUMBER: 09 SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 555
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                                                                            Matches
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                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Dermatophagoides farinae
                                                                                                                                                                  TYPE: PRT ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                ENGTH: 490
                                                                                            Local
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153 DKONYLTLVRELK 165
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                                  1 DKONYLALVRELK 13
                                                                          l Similarity
12; Conserv
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                                                                                            93.8%;
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                                                                                            Score 60; DB 4;
Pred. No. 0.0095;
                                                                            Mismatches
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                                                                                                              DB 4; Length 490;
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                                                                            Indels
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US-09-292-225-35
; Sequence 35, Applicat
; Patent No. 6455686
; GENERAL INFORMATION:

Application US/09292225

APPLICANT: McCall, Catherine A.

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EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 38
LENGTH: 509
TYPE: PAT
ORGANISM: Dermatophagoides farinae
US-09-292-225-38
RESULT 8
US-09-489-039A-12116
; Sequence 12116, Application US/09489039A
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; ORGANISM: Dermatophagoides farinae
US-09-292-225-35
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CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 199-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS INTLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hunter, Shirle
APPLICANT: Weber, Eric R.
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No. 6455686
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iilarity 92.3%;
Conservative
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Pred. No. 0.0099;
                                                                                                                                                                                          Score 60; DB 4;
Pred. No. 0.0099;
0; Mismatches
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 12116
LENGTH: 611
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
FRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR BILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR SEQ ID NOS: 14342
                                                                                                                                                   STATE: D.C.

STATE: D.C.

ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
15-NOV-1991
CLASSIFICATION: 530
PRIOR APPLICATION: 530
ATTORNET/AGENT INFORMATION:
NUMBER: DOLLET Jane F. R.
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods
TITLE OF INVENTION: Determinant
                                            NAME: POTTEY: Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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50.0%;
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Pred. No.
                                                                                               03495.0106-03000
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SEQUENCE CHARACTERISTICS: LENGTH: 289 amino acid

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Best Local Similarity
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                                                                                                                                             ; MOLECULE TYPE: peptide US-08-481-985B-79
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US-08-481-985B-79
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ALITITLE OF INVENTION:
NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
ADDRESSEE:
STREET: 130
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                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 03
                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                      LENGTH:
119
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                                DKONYLALVRELK 13
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1300 I Street, N.W., Suite 700
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Kourilsky, Phillipe
VENTION: Altered Major Histocompatibility Complex
                                                                                                                                                                                                                      289 amino acids
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                                                                      Conservative
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53.8%;
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Pred. No.
                                                                                      Score 39;
Pred. No.
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                                                                      Mismatches
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27;
                                                                                                         DB 3;
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                                                                 Gaps
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RESULT 11

US-09-052-778-2

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GENERAL INFORMATION:

APPLICANT: BYANT, PETEY J.
APPLICANT: KAWAMMIYA, KAZUO
TITLE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS
TITLE OF INVENTION: OF USE

Sequence 2, Application US/09052778A Patent No. 6060590

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                                           Query Match
Best Local Similarity
"~+~hes 7; Conserva
                                                                                                                       ; MOLECULE TYPE: peptide US-08-370-476-79
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                                                                                                                                                                                                                TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-DEC-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIILE OF INVENTION: Altered Major Histocompatibility Complex
IIILE OF INVENTION:
                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                                                                         NAME: Meyers, Kenneth
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 15-NO
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119 DGQDYTALMEDLK 131
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                             DKONYLALVRELK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                               289 amino acids
                                                           Conservative
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                                                                           Score 39; DB 3; Pred. No. 27;
                                                             Mismatches
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                                                                                         Length 289
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                                                           Gaps
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CURRENT APPLICATION NUMBER: US/09/052,778A; CURRENT FILING DATE: 1998-03-31; NUMBER: FastSEQ for Windows Version 4.0; SEQ ID NO 2; SEQ ID NO 2; LENGTH: 442; TYPE: PRT
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US-09-107-532A-4886
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                                                   US-09-107-532A-4886
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GENERAL INFORMATION:
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Best Local (
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                               TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4886:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...333
SEQUENCE DESCRIPTION: SEQ ID NO: 4886:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                  HYPOTHETICAL: YI ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT
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                                                                                                                    FEATURE:
                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194
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8; Conserv
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OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                   LENGTH: 333 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATA:
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                                                                                                                                                                   YES
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57.8%;
72.7%;
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Pred. No.
 Score
Pred.
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 No.
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 DB
71;
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                 Length 333;
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEG ID NOS: 5674
SEQ ID NO 4256
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US-09-134-001C-4356
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                                                                                                                                     ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30217
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US-09-252-991A-30217
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SEQ ID NO 30217
LENGTH: 191
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30217, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                             PRIOR FILING DATE:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
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S52422

Chitinase (EC 3.2.1.14) B precursor - Serratia marcescens (strain C)species: Serratia marcescens

C, Species: Serratia marcescens

A; Variety: strain BuL200

C; Accession: S52422

R; Brurberg, M.B.; Eijsink, V.G.H.; Haandrikman, A.J.; Venema, G.; Microbiology 141, 13-131, 1995

A; Title: Chitinase B from Serratia marcescens BuL200 is exported A; Reference number: S52422; MUID:95202070; PMID:7894703

A; A; Accession: S52422
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## ALIGNMENTS

Serratia marcescens (strain BJL200)

03-Nov-1995 #text\_change 08-Oct-1999

A.J.; Venema, G.; Nes, I.F.

to the periplasm withou

Query Match 73.5%; Score 61; DB 2; Length 499;	A;Gene: chiB A;Gene: chiB C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;42-499/Product: chitinase B #status predicted <mat></mat>	A;Residues: 1-499 <har> A;Cross-references: EMBL:X15208; NID:g47227; PIDN:CAA33278.1; PID:g47228 A;Experimental source: strain QMB1466 C.Genetics:</har>	Nucleic Acids Res. 17, 5395, 1989 Nucleic Acids Res. 17, 5395, 1989 A; Title: Nucleotide sequence of the chitinase B gene of Serrat: A; Reference number: \$04856; MUID:89345110; PMID:2668886 A; Accession: \$04856 A; Molecule type: DNA		precursor - scens	Qy 2 KINMGVPFYGRA 13  :         Db 284 KINMGVPFYGRA 295	Query Match 73.5%; Score 61; DB 2; Length 499; Best Local Similarity 91.7%; Pred. No. 0.0074; Matches 11; Conservative 1; Mismatches 0; Indels	C;eenetics: A;Gene: chiB C;Keywords: glycosidase; hydrolase; polysaccharide degradation	A; Accession: 032422 A; Molecule type: DNA A; Residues: 1-499 <bru> A; Cross-references: EMBL: Z36295; NID: g677860; PIDN: CAA85292.1; PID: g677861 A; Experimental source: strain BJL200</bru>
	ride degradation d <mat></mat>	IDN:CAA33278.1; PID:g47228	B gene of Serratia marcescens QMB1466. D:2668886	1990	Serratia marcescens (strain QMB1466)		2; Ler 074; 0;	ride degradation	PIDN:CAA85292.1; PID:g677861

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chitinase (EC 3.2.1.14) precursor - Bacillus circulans
C;Species: Bacillus circulans
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R,Lightning, J.
submitted to the EMBL Data Library,
A,Reference number: Z19950
A,Accession: T24898
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A;Note: sequence extracted from NCBI backbone (NCBIN:136417, N:C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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A;Molecule type: mRNA
A;Residues: 1-554 <KRA>
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A;Title: Sequence of a CDNA and expression of the gene encoding A;Reference number: A56596; MUID:93357793; PMID:8353525
A;Accession: A56596
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                   C;Accession: A38368
R;Watanabe, T.; Suzuki, K.; Oyanagi, I
J. Biol. Chem. 265, 15659-15665, 1990
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C;Accession: A56596
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Species: Manduca sexta (tobacco hornworm)
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Best Local :
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Chem. 265, 15659-15665, 1990
Gene cloning of chitinase Al
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Pred. No. 0.02
6; Mismatches
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Pred. No. 0.073;
1; Mismatches
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                                         W.; Ohnishi, K.; Tanaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
     from Bacillus circulans WL-12
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RESULT 6
G84238
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D83764
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M57601; GB:J05599; NID:g1066341; PIDN:AAA81528.1; PID:g142688 C;Superfamily: fibronectin type III repeat homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                            C;Accession: D83764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Vng0818c [imported] - Halobact C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001
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A; Residues: 1-699 <WAT>
                                                                                                      A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04635.1; A;Experimental source: strain C-125
                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-599 <STO>
                                                                                                                                                                                                                                                                                               chitinase BH0916 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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A; Residues: 1-572 <S
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                                                                       A;Gene:
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thauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C
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Pred. No. 0.08
1; Mismatches
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Pred. No.
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KLVLGMPFYGRGWS

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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler leth, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Latrdinois, A.; Latrdinois, A.; Latrdinois, A.; Lardinois, A.; Coliega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, A.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seroy A.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A. A.; Fitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 31-36;87-112;252-275;282-305;337-371 <HEW>
C;Superfamily: Streptomyces chitinase chi40
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;Keywords: signal sequence #status predicted <SIG>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-371/Product: chitinase/lysozyme PZ #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Gen. Genet. 245, 245-254, 1374
A;Title: Molecular characterization of a novel tobacco pathogenesis-related A;Reference number: S51591; MUID:95115673; PMID:7816033
A;Accession: S51591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X78325; NID:g467688; PIDN:CAA55128.1; PID:g467689
A;Experimental source: cv. Samsun NN
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A; Residues: 1-378 < HEI>
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A; Residues: 1-232 < KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Species: Nicotiana tabacum (common tobacco)
;Pate: 15-Jul-1995 #sequence revision 08-Sep-1995 #text_change 22-Jun-1999
;Paccession: S51591; S51332; S43119
;Heitz, T.; Segond, S.; Kauffmann, S.; Geoffroy, P.; Prasad, V.; Brunner, F.; Fritig, Jol. Gen. Genet. 245, 246-254, 1994
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Best Local S
Matches 9
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KLVMGVPFYGRA 13
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Pred. No.
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Pred. No.
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R;Arias, B.B.; Verhage, H.G.; Jaffe, R.C.
Biol. Reprod. 51, 685-694, 1994
A;Title: Complementary deoxyribonucleic acid cloning and molecular characterization
A;Reference number: 138605; MUID:95119256; PMID:7819450
                                                                                                                                                      I38605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-457 <SHA>
A;Cross-references: DDBJ:AF009354
C;Comment: This enzyme cleaves the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 208, 315-322, 1998
A;Title: The Ld Chtl gene encodes the secretory chitinase A;Reference number: JC6551; MUID:98201628; PMID:9524285 A;Accession: JC6551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chitinase (EC 3.2.1.14) precursor - Leishmania donovani
C;Species: Leishmania donovani
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
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C;Genetian:
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A;Title: Chitinases are a multi-gene family in Aedes, A;Reference number: 217872
A;Accession: T14075
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                                                                                          C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998
                                                                                                                                                                                                                                                                                                                                                                                     F;1-19/Domain: signal sequence #status predicted <SIG>F;20-457/Product: chitinase #status predicted <MAT>F;384/Binding site: carbohydrate (Asn) (covalent) #sta
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C;Keywords: glycoprotein; glycosidase; glycosyltransferase; hexosyltransferase; hydrolas:
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R; Shakarian, A.M.; Dwyer, D.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            618/1; 951/3; 1151/2 hydrolase; polysacch
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72.7%;
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Pred. No. 1;
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Pred. No. 0.4;
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A;Accession: I38605
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-654 <RES>
                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-383 <SHA>
A;Cross-references: EMBL.Z47803; NID:9634097; PIDN:CAA87764.1; PID:9634098
C;Superfamily: Streptomyces chitinase chi40
                                                                                                                                                                                                                                                                                                        C;Accession: S51327
R;Shackelton, L.M.; Mann, D.M.; Millis, A.J.T.
submitted to the EMBL Data Library, January 1995
A;Description: Identification of a 38kDa heparin-binding glycoprotein (gp38k) in differen
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submitted to the EMBL Data Library, September 1996
A;Description: The sequence of C. elegans cosmid T01C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U09550; NID:g529147; PID:g529148
                                                                                                                                                                                                                                                               A;Reference number: S51327
A;Accession: S51327
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;Species: Sus scrofa domestica (domestic pig)
;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Molecule type: DNA
;Residues: 1-1484 <GRA>
;Cross-references: EMBL:U70858; PIDN:AAB09177.1; GSPDB;GN00023; CESP:T01C4.1
;Experimental source: strain Bristol N2; Clone T01C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPOThetical protein T01C4.1 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Map position: 5;Introns: 60/1; 179/1; 219/3; 392/3; 481/3; 549/2; 594/2; 736/3; 843/3; 1056/2; 1444/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: CESP:T01C4.1
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252 NKLVMGIPTFGRSFTL 267
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                                    1 DKLVMGVPFYGRAXSI 16
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Pred. No. 1.4;
1; Mismatches
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Search completed: March 22, Job time : 1.10561 secs

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07:01:26

RESULT 15 JC4565

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A;Introns: 47/3; 171/3; 191/3; 215/2; 393/3
(C;Superfamily: Streptomyces chitinase chi40
C;Keywords: glycomyces; pydroidase; polysaccharide degradation
C;Keywords: signal sequence #status predicted <SIG>
F;18-17/Domain: signal sequence #status predicted <MAT>
F;387/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Isolation and characterization of two chitinase-encoding genes (cts1, cts2) A;Reference number: JC4565; MUID:96144270; PMID:8566773 A;Accession: JC4565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: JC4565
R;Pishko, E.J.; Kirklan
Gene 167, 173-177, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chitinase (EC 3.2.1.14) 1 precursor - Coccidioides immitis
N;Alternate names: complement fixation antigen homolog; CTS1 protein
C;Species: Coccidioides immitis
C;Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
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A;Experimental source: C735
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                                                                                                 Matches
                                                                                                                                             Query Match
284 NKIVLGMPLYGRA 296
                                               1 DKLVMGVPFYGRA 13
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                                                                                                                         Similarity
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                                                                                                 Conservative
                                                                                                                       60.2%;
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Pred. No. 0.56;
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homo sapien clostridium

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Total number of hits satisfying chosen parameters:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 2000000000
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1357.597 Million cell updates/sec
       P36909
Q15782
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InterPro; IPR003610; CBM_5_12.
InterPro; IPR0013623; GlyGo_hydro_18.
InterPro; IPR001579; GlyGo_hydro_18AS.
InterPro; IPR001579; GlyGo_hydro_18; 1.
Pfam; PF002839; CEM_5_12; 1.
Prome; PB00704; GlyGo_hydro_18; 1.
Prome; PB0070471; GlyGo_hydro_18; 1.
SMART; SM00495; ChtBD3; 1.
SMART; SM00495; CHED3; 1.
PROSITE; PS01095; CHITINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P11797;
01-OCT-1989
01-OCT-1989
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       2170.";

J. Bacteriol. 179:7111-7117(1997).

-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-ectvl-D-glucosamine polymers of chitin.

Acetvl-D-glucosamine polymers of chitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98037511; PubMed=9371460; Watanabe T., Kimura K., Sumiya T., Nikaidou N., Suzuki K., Suzuki M., Taiyoji M., Ferrer S., Regue M.; "Genetic analysis of the chitinase system of Serratia marcescens 2170.";
                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRALN=ATCC 990 / QMB1466;
MEDLINE=89345110; PubMed=2668886;
Harpster M.H., Dunsmuir P.;
Harpster M.H., Dunsmuir P.;
"Nucleotide sequence of the chitinase B
"Nucleotide sequence of the chitinase B
QMB1466.";
                                                                                                                                                                               EMBL; X15208; CAA33278.1; -.
EMBL; AB015997; BAA31568.1; -.
PIR; S04856; S04856.
HSSP; P07254; 1CTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=2170;
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(Rel. 12, Last sequence update)
(Rel. 39, Last annotation updat
precursor (BC 3.2.1.14).
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CHIT NPVOP
POLG HCVJT
POLG HCVJ
POLG HCVJ
POLG HCVJ
POLG HCVJ
LOCZ MOUSE
DPOZ HUMAN
CHIT NPVAC
LUCI VARHI
DPOZ YEAST
CHIA HUMAN
TETX_CLOTE
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Q000266
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ACT_SITE
SEQUENCE
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236362;

01-JUN-1994 (Rel. 29, Created)

01-JUN-1994 (Rel. 29, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Endochitinase precursor (EC 3.2.1.14).

Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MANSE
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97215580; PubMed=9061927;
Choi H.K., Choi K.H., Kramer X.J., Muthuk
"Isolation and characterization of a geno
insect molting enzyme, Chitinase.";
Insect Biochem. Mol. Biol. 27:37-47(1997)
                                                                          InterPro;
InterPro;
InterPro;
                                                                                                                                                     EMBL; U02270; AAC04924.1; -.
EMBL; L49234; AAB53952.1; -.
PIR; A56596; A56596.
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93357793; PubMed=8353525;
Kramer K.J., Corpuz L., Choi H.K., Muthukrishnan S.
"Sequence of a cDNA and expression of the gene enco
gut chitinases of Manduca sexta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insect Biochem. Mol. Biol. 23:691-701(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAPALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-CAPALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-CAPALYTIC ACTIVITY: Belonges of Chitin.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Epidermis and gut.

DEVELOPMENTAL STAGE: High levels seen in the epidermis on day 0, but rapidly disappears and is undetected on days 1-4 of fifth instar. It reappears on day 5 and peaks on day 7 after which a rapid decline is seen. In the gut is detected on day 6 with lower levels seen on days 0, 7 and 8.

SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 chitin-binding type-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Digest chitin
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                   Pro; IPR002557; Chitin bind PerA.
Pro; IPR001223; Glyco hydro 18.
Pro; IPR001579; Glyco hydro 18AS.
PF001607; CBM 14; 1.
PF000704; Glyco hydro 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
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11; Conservative
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Best Local
This SWISS-PROT entry is copyright. It is produced through a content the Swiss Institute of Bioinformatics and the EMEL of the European Bioinformatics Institute. There are no restrictions in the produced and this statement is modified and this statement is not removed. Usage by and a license agreement 'Content is entitles requires a license agreement 'Content in the statement is a long as its content is entitle requires a license agreement 'Content in the statement is entitle of the statement in the statement is entitle or requires a license agreement 'Content in the statement in the statement in the statement is entitle or requires a license agreement 'Content in the statement in the statement is entitle or require a license agreement 'Content in the statement is entitle or require a license agreement 'Content in the statement is entitle or require a license agreement in the statement is entitle or require a license agreement in the statement is entitle or require a license agreement in the statement is entitle or require a license agreement in the statement in the statement is entitle or require a license agreement in the statement in the statement is entitle or require and the statement in t
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable chitinase 3 (EC 3.2.1.14).
CHT3 OR CG18140.
Drosnowhin - -
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Q9W5U2; 017422;
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10-OCT-2003 (Rel
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CARBOHYD
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PROSITE; PS50940; CHITINASE 18; 1.
PROSITE; BS01095; CHITINASE 18; 1.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98324849; PubMed=9662472; de la Vega H., Specht C.A., Liu Y., "Chitinases are a multi-gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
MEDLINE=22426071; PubMed=12537574;
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SMART; SM00636; Glyco_1
                                                                                                                                                                                                                                                                                                                                                                                             Insect Mol. Biol. 7:233-239(1998).

-|- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages acetyl-D-glucosamine polymers of chitin.

-|- SIMILARITY: Belongs to chitinase class II (family 18 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 182-294
STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Heterochromatic sequences assembly.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SER/THR-RICH.
SER/THR-RICH.
CHITIN-BINDING TYPE-2
PROTON DONOR (BY SIMI
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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RESULT 4
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Best Local Similarity
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R InterPro; IPR001257; ChitIn bind PerA.

R InterPro; IPR001257; ChitIn bind PerA.

R InterPro; IPR001223; Glyco_hydro_18.

R InterPro; IPR001279; Glyco_hydro_1885.

R Pfam; PF00407; CBM_14; 2.

R Pfam; PF00704; Glyco_hydro_18; 1.

R Pr0Dom; PF007041; Glyco_hydro_18; 1.

R Pr0Dom; PF007041; Glyco_hydro_18; 1.

R PR0DOM; SMART; SM00494; ChtBD2; 2.

R SMART; SM00636; Glyco_18; 1.

R SMART; SM00636; Glyco_18; 1.

R PROSITE; PS01095; CHITINASE_18; FALSE_NEG.

R PROSITE; PS01095; CHITINASE_18; FALSE_NEG.

Hydrolase; Glycosidase; Chitin degradation; Chitin-binding;
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01-FEB-1991
10-OCT-2003
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P20533;
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DOMAIN
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295
SEQUENCE
458 AA; 52330 MW;
                                                                                                                                                                                                                                           STRAIN=WL-12;
MEDLINE=93366760; PubMed=8103047;
Watanabe T., Kohori K., Miyashita
Uchida M., Tanaka H.;
                                                                                                                                                                                                                 "Identification of glutamic acid 204 and chitinase Al of Bacillus circulans WL-12
                                                                                                                                                                                                                                                                                                                "Gene cloning of chitinase Al from Bacillus circulans WL-12 its evolutionary relationship to Serratia chitinase and to t III homology units of fibronectin.";
J. Biol. Chem. 265:15659-15665(1990).
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90368776; PubMed=2203782;
                                                                                                                                                                                                   chitinase activity.";
                                                                                                                                                                                                                                                                                                       MUTAGENESIS
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                                                                                                                                                                                        Biol.
                                                                                                                          Biol. Chem. 268:18567-18572(1993).

CAPALTYIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages acetyl-D-glucosamine polymers of chitin.

SIMILARITY: Contains 2 fibronectin type III domains.

SIMILARITY: Belongs to chitinase class II (family 18 of
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(Rel. 17,
(Rel. 42,
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Pred. No. 0.02
5; Mismatches
                 is not removed. Usage by and for agreement (See http://www.isb-sib.cl
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CHITIN-BINDING TYPE-2 2.
PROTON DONOR (BY SIMILARITY)
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REPORT OF SERVICE SERV
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Best Local S
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Pfam; PF00041; fn3; 2.

Pfam; PF00704; Glyco hydro 18; 1.

ProDom; PD000471; Glyco hydro 18; 2.

SMART; SM00405; ChtBD3; 1.

SMART; SM00606; FN3; 2.

SMART; SM00606; FN3; 2.

SMART; SM00636; Glyco 18; 1.

PROSITE; PS01095; CHITINASE 18; 1.
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Berkeley;
MEDLINE=22426071; F
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DOMAIN
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SEQUENCE
                                                                                                                                                                                                           MEDLINE-22426071; PubMed=12537574;
Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin Karpen G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
PIR; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003610; CBM_5_12.
InterPro; IPR008957; PN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Pfam; PF02839; CBM_5_12; 1.
                                                        MEDLINE=98324849; PubMed=9662472; de la Vega H., Specht C.A., Liu Y
                                                                                              SEQUENCE OF
STRAIN=Canto
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                    "Chitinases are a multi-gene
                                                                                                                                                      Genome
                                                                                                                                                                                             "Heterochromatic sequences in a Drosophila whole-genome
                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prosophila melanogaster
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                                                                                                                                                      Biol.
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ea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycosidase;
                                                                                                                    151-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                      3:RESEARCH0085.1~RESEARCH0085.16(2002)
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Chitin d
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fruit
                                                                                                                  z
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CATALYTIC.
FIBRONECTIN TYPE-III (R-1).
FIBRONECTIN TYPE-III (R-2).
FROTON DONOR (PROBABLE).
D-N: DECREASE IN ACTIVITY.
D-E: NO CHANGE IN ACTIVITY.
E-D/Q: LOSS OF ACTIVITY.
AC7C9B22E2987643 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB
Pred. No. 0.04
1; Mismatches
                                      family
                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      degradation; Signal; Repeat;
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                                      ij
                                                        Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508
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                                    Aedes, Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
0.044;
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                                                                                                                                                                                           shotgun
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGP PAPAN STANDARD; PRT; 623 AA.
P36718;
D1-JUN-1994 (Rel. 29, Created)
D1-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last amotation update)
Oviduct-specific glycoprotein precursor (Oviduct
(Oviductin) (Estrogen-dependent oviduct protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PlyBase; FBgn0022703; Cht1.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001279; Glyco_hydro_18AS.
Pfam; PP00704; Glyco_hydro_18; 2.
ProDom; PD000471; Glyco_hydro_18; 2.
ProDom; PD000471; Glyco_hydro_18; 2.
PNART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHTTINASE_18; 1.
PROSITE; PS01095; CHTTINASE_18; 1.
Hydrolase; Glycosidase; Chitin degradation; Multigene family.
ACT_SITE 264 264 PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                       Verhage H.G., Fazleabas A.T., Mavrogianis P.A., O'Day-Bowman M.B., Donnelly K.M., Arias E.B., Jaffe R.C., "The baboon oviduct: characteristics of an oestradiol-dependent oviduct-specific glycoprotein.", thum. Reprod. Update 3:541-552(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                         "Cloning of a recombinant complementary DNA to a baboon (Pap anubis) estradiol-dependent oviduct-specific glycoprotein.", Mol. Endocrinol. 5:356-364 (1991).

-I- FUNCTION: Binds to occyte zona pellucida in vivo. May pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OVGP1 OR OGP.
Papio anubis (Olive baboon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF026500; AAB81858.1; -.
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                                                                                                                                                                       MEDLINE-91367180; PubMed=1716345;
Donnelly K.M., Fazleabas A.T., Ve
                                                                                                                                                                                                                                                                                                                                      MEDLINE=98244335; PubMed=9584944;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9555;
                                                                                                                                                                                                                           PRELIMINARY PARTIAL SEQUENCE FROM
         in the fertilization process and/or early SUBCELLULAR LOCATION: Secretory granules. TISSUE SPECIFICITY: Oviduct. DEVELOPMENTAL STACE: At the time of ovulate. SIMILARITY: Belongs to family 18 of glycos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acetyl-D-glucosamine SIMILARITY: Belongs thydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of acetyl-D-glucosamine polymers of chitin.
SIMILARITY: Belongs to chitinase class II (family 18 of gl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378
                                                                                                                                                             R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
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                                                                                                                                                                                                                                                                                                                                                                                                                      Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57751 MW;
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Pred. No. 0.07
4; Mismatches
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           of ovulation.
of glycosyl hydrolases
                                                                                                                                                                       H.G., Mavrogianis
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0.071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Oviductal
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                                                                             embryonic
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                                                                                           vivo. May play a role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein)
                                                                                                                                           (Papio
                                                                               development.
                                                                                                                                                                          P.A.,
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Best Local S
Matches 8
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InterPro; IPR001223; Glyco_hydro_18AS.
InterPro; IPR001273; Glyco_hydro_18AS.
InterPro; IPR001579; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_hydro_18; 1.
SMART; SM00636; GlYco_hydro_18; 1.
SMART; SM01635; CHITINASE_18; FALSE_NEG.
Glycoprotein; Fertilization; Signal.
Glycoprotein; Fertilization; Signal.
SIGNAL
SIGNAL
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SIGNAL
CARBOHYD 402 402 N-LINKED (GLCNA
CARBOHYD 401 441 N-LINKED (GLCNA
CARBOHYD 401 441 N-LINKED (GLCNA
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                               Jaffe R.C.
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q12889; Q15841;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein) (Mucin 9).
OVGP1 OR OGP OR MUC9.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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                                                                                                                                  Coville G.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               glycoprotein.
Biol. Reprod.
                                                                                                                                                                                                                                                                                                              MEDLINE-95119256; PubMed-7819450;
Arias E.B., Verhage H.G., Jaffe R.C.;
"Complementary deoxyribonucleic acid
characterization of an estrogen-depen
This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OGP HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M59903; AAB39765.1; -.
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                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANT GLN-676.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                 SSUE=Oviduct
                                                           FUNCTION: Binds to occyte zona pellucida in vivo. May pl
in the fertilization process and/or early embryonic deve
SUBCELLULAR LOCATION: Secretory granules.
TISSUE SPECIFICITY: Oviduct,
SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
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8; Conser
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                                                                                                                                                                                                                                                                               51:685-694(1994).
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66.7%;
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BY SIMILARITY.
OVIDUCT-SPECIFIC GLYCOPROTEIN.
N-LINKED (GLCNAC. . .) (POTENT
N-LINKED (GLCNAC. . .) (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9E21CE481FFF1268 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
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                                                                                                               ay play a role development.
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                collaboration -
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RESULT 8
OGP MOUSE
ID OGP MOUSE
AC Q62010;
DT 01-NOV-199;
DT 28-FEB-200;
DE CViduct-spe
DE (CViductin)
GN OVGP1 OR OC
OS Mus muscult
OC Eukaryota;
OC Mammalia;
EC MAMMERICE;
RF SEQUENCE FF
RC STRAIN=1CR;
RA Araki Y;
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RA Araki Y;
RA Araki Y;
RA Sendai Y;
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GO; GO:0007565; P:pregnancy; TAS.

InterPro; IPR001223; Glyco_hydro_18.

InterPro; IPR001579; Glyco_hydro_18AS.

Pfam; PF00704; Glyco_hydro_18; 1.

ProDom; PD000471; Glyco_hydro_18; 1.

R SMART; SM00636; Glyco_18; 1.

R PROSITE; PS01095; CHITINASE 18; FALSE NE

R PROSITE; PS01095; CHITINASE 18; FALSE NE

Glycoprotein; Pertilization; Signal; Pol

W Glycoprotein; Pertilization; SIGNAL; Pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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SIGNAL
CHAIN 2
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CONFLICT
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or send a
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                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal (Oviductin) (Estrogen-dependent oviduct protein).
OVGP1 OR OGP OR CHIT5.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
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CARBOHYD
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 "Molecular cloning and charact glycoprotein.";
Biol. Reprod. 53:285-294(1995)
                                                            STRAIN=ICR; TISSUE=Oviduct;
MEDLINE=96115001; PubMed=7492680;
Sendai Y., Komiya H., Suzuki K.,
                                                                                                                                        Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L; U58010; AAB04126.1; JOINED.
L; U58001; AAB04126.1; JOINED.
L; U58002; AAB04126.1; JOINED.
L; U58003; AAB04126.1; JOINED.
L; U58004; AAB04126.1; JOINED.
L; U58006; AAB04126.1; JOINED.
L; U58006; AAB04126.1; JOINED.
L; U58007; AAB04126.1; JOINED.
L; U58007; AAB04126.1; JOINED.
L; U58009; AAB04126.1; JOINED.
L; U58009; AAB04126.1; JOINED.
L; U58009; AAB04126.1; JOINED.
L; JU58009; AAB04126.1; JOINED.
L; JUS8009; AAB04126.1; JOINED.
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6768
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Rodentia;
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                                  characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n; Signal; Folymorphism.

BY SIMILARITY.

OVIDUCT-SPECIFIC GLYCOPROTEIN.

OVIDUCT-SPECIFIC GLYCOPROTEIN.

N-LINKED (GLCNAC...) (POTENTIAL).

FINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

S-9 (in dbsnp:7825).

/FTIdeVAR 0.16109.

S-9 F (IN REF. 2).

S-9 F (IN REF. 2).
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Pred. No. 0.32;
                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae
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                                                                Kikuchi
                                                                                                                                                             Muridae;
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                                  mouse
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; Murinae; Mus
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Best Local S
Matches
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01-OCT-1996
01-OCT-1996
10-OCT-2003
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
         SEQUENCE FROM N.A.
STRAIR-Silveira;
Yang C., Zhu Y., Magee D.M., Cox R.A.;
Yang C., Zhu Y., Magee D.M., Cox R.A.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages
acetyl-D-glucosamine polymers of chitin.
-!- SIMILARITY: Belongs to chitinase class II (family 18 of hydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
Glycoprotein; Fertilization; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                Coccidioides posadasii.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; E
Onygenales; mitosporic Onygenales; Coccidioides
                                                                                                                                                                                                                                                                                                                                                                                                  COCPO
                                                                                                                                         MEDLINE=96144270; PubMed=8566773;
Pishko E.J., Kirkland T.N., Cole G.T.;
"Isolation and characterization of two chi
(ctsl, cts2) from the fungus Coccidioides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D32137; BAA06863.1; -. MGD; MGI:106661; Ovgp1.
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                                                                                                                               Gene 167:173-177(1995).
                                                                                                                                                                                                                                                                                                                   Endochitinase
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                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                       (CF-antigen)
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in the fertilization process and/or early embryonic deve
SUBCELLULAR LOCATION: Secretory granules.
TISSUE SPECIFICITY: Epithelial cells of the oviduct.
SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                     COCPO
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3 (Rel. 42, Last a
ase 1 precursor (E
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721 AA;
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78807 1
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75.0%;
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                                                                                                                                                                                                                                                                                                                   sequence update)
annotation update)
(EC 3.2.1.14) (Complement-fixation antigen)
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Pred. No. 0.34
1; Mismatches
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OVIDUCT-SPECIFIC GLYCOPRO
21 X 7 AA TANDEM REPEATS

[TAP]-G-[[V]]...
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0.34;
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REPEATS OF S-
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or send an email to license@isb-sib.ch).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGL1_HUMAN STANDARD; PRT; 383 AA.
236222; P30923;
01-JUL-1993 (Rel. 26, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Chithnase-3 like protein 1 precursor (Cartilage glycoprotein-39) (GP-Chithnase-3 like protein) (YKL-40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; 1.
PROSITE; PS01095; CHITINASE_18; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHI3L1
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                                                               Rehli M., Krause S.W., Andressen R.;
"Molecular characterization of the gene for human cartilage gp-39 (CHIJL1), a member of the chitinase protein family and marker for late stages of macrophage differentiation.";
Genomics 43:221-225(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                              "Hakala B.E., White C., Recklies A.D.;
"Human cartilage gp-39, a major secretory product of articular chondrovytes and synovial cells, is a mammalian member of a chiprotein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Cartilage;
MEDLINE=94064658; PubMed=8245017;
                                                                                                                                                                                                                                                  MEDLINE=97386591; PubMed=9244440;
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                                                                                                                                                                                                                                                                                           rissue=Blood;
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SL; U51271; AAA96515.1; -.
SL; U33265; AAB6687.1; -.
S; IDZK; 27-SEP-00.
S; ILL4; 25-SEP-02.
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1LL7; 18-DEC-02.
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8; Conserv
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427 AA;
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-LINKED (GLCANCI...) (POTENTIAL).

RWLSLRCLFCELGREMETILSTVTAVTVVTDDIO -

SMSSMPNYYPVPBAPEGGFRSVVYFVNW (IN RE
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Pred. No. 0
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RESULT 11
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Best Local S
Matches 8
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EMBL; Y08374; CAA69661.1; JOIN
EMBL; Y08375; CAA69661.1; JOIN
EMBL; Y08376; CAA69661.1; JOIN
EMBL; Y08377; CAA69661.1; JOIN
EMBL; Y08378; CAA69661.1; JOIN
EMBL; Y08378; CAA69661.1; JOIN
EMBL; Y08378; CAA69661.1; JOIN
EMBL; Y08378; CAA6967.1; JOIN
                                                                                                                                                                                                                    Q01459;
01-JUL-1993
01-JUL-1993
10-CCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
InterPro; IPR001223; Glyco hydro_18.
InterPro; IPR001579; Glyco hydro_18AS.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_hydro_18; 1.
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human synovial cells secrete a 39 kDa protein similar to mammary protein expressed during the non-lactating period. Biochem. J. 269:265-268(1990).
                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
10-CCT-2003 (Rel. 42, Last ann
Di_N-acetylchitobiase precurso
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MEDLINE=90328983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:1932; CHI3L1.
                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                         CTBS
                                                                                                                                                                                                                                                                                                                      DIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
SIGNAL
                                                                    NCBI_TaxID=9606
                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: May play an important role in the capacity of ce respond to and cope with changes in their environment. SUBCELLULAR LOCATION: Extracellular. TISSUE SPECIFICITY: Present in articular chondrocytes, syncells as well as in liver. Undetectable in muscle tissues, pancreas, mononuclear cells, or fibroblasts.

PTM: Glycosylated.
                                                                                                                                                                                                                                                                                                                      HUMAN
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                                                                                                                                                                         OR CTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                             253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIVMGVPFYGRAXSI 16
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60
383
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                                                                                                                                                                                                                                                                                                                      STANDARD;
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383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 N
42613 MW;
                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%;
                                                                                                                                                                                        Last sequence update)
Last annotation update)
precursor (EC 3.2.1.-).
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; JOINED.
; JOINED.
; JOINED.
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Pred. No. 0.41;
5; Mismatches
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N-LINKED (GLCNAC. . .) (PO:
; 76ADD8298EEEC2D1 CRC64;
                                                                                                                                                                                                                                                                                                                         385
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در
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SEQUENCE FROM N.A. TISSUE=Placenta;

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EMBL; AFUL.

EMBL; AFUL.

PIR; A44102; A.

Genew; HGNC:2496; C...

MIN; 600873; -...

R InterPro; IPR001223; Glyco_hydro_10...

IR PrODOM; PD000471; Glyco_hydro_18; 1.

DR PrODOM; PD000471; Glyco_hydro_18; 1.

DR PRODOM; PD000471; Glyco_hydro_18; 1.

PR PRODOM; PD000471; Glyco_hydro_18; 1.

DR PRODOM; PD000471; Glyco_bydro_18; 1.

PR PRODOM; PD000471; Glyco_hydro_18; 1.

PR PRODOM; PD000471; Glyco_hydro_18; 1.

PR SIGNAL 39 385

PROTON DONGR (BY SIMILARITY).

P
                              AC Q60557; Q60526;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 07-viduct-specific glycoprotein precursor (Ovidence of the content o
RESULT
OGP MES
OF MES
AC Q6
DT 01
DT 115
DT 15
CGN 0V
DE (C
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EMBL; AF085706; AAC35852.1; JOINED.
EMBL; AF085700; AAC35852.1; JOINED.
EMBL; AF085701; AAC35852.1; JOINED.
EMBL; AF085702; AAC35852.1; JOINED.
EMBL; AF085703; AAC35852.1; JOINED.
EMBL; AF085704; AAC35852.1; JOINED.
EMBL; AF085705; AAC35852.1; JOINED.
EMBL; AF085705; AAC35852.1; JOINED.
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Liu B., Ahmad W., Aronson N.N. Jr.;
"Structure of the human gene for lysosomal di-N-acetylchitobiase.";
Glycobiology 9:589-593(1999).
-!- FUNCTION: Involved in the degradation of asparagine-linked glycoproteins. Hydrolyze of N-acetyl-beta-D-glucosamine (1-4)N-acetylglucosamine chitobiose core from the reducing end of the bond, it requires prior cleavage by glycosylasparaginase.
-!- SUBCELLULAR LOCATION: Lysosomal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92406917; PubMed=1527079; Fisher K.J., Aronson N.N. Jr.; Fisher K.J., Aronson N.N. of the cDNA sequence encoding the lysosomal "Cloning and expression of the cDNA sequence encoding the lysosomal glycosidase di-N-acetylchitoblase."; J. Biol. Chem. 267:19607-19616(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.
   Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLVMGVPWYG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLVMGVPFYG 11
   auratus
   (Golden hamster)
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                                                                                                                                           update)
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Glycoprotein;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            zona pellucida-binding glycoprotein.";

Blochem. J. 295:437-445(1993).

i- FUNCTION: Binds to occyte zona pellucida in vivo. May play a rol. in the fertilization process and/or early embryonic development. Might act as a protective secretion influencing the first steps the reproductive process necessary for the normal triggering of fertilization and early embryonic development.

i- SUBCELLULAR LOCATION: Secretory granules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paquette )
Submitted
           REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
CARBOHYD
CARBOHYD
                                                                                                                                                                EMBL; U15048; ANDESERVA; CONTROLES.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_1885.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paquette Y., Merlen Y., Malette B., Bleau G.;
"Allelic polymorphism in the hamster ovdductin variable number of mucin-like tandem repeats.";
Mol. Reprod. Dev. 42:388-396(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein.";
Biol. Reprod. 5
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Suzuki K., Sendai Y., Onuma T., Hoshi H., Hiroi M., Araki
"Molecular characterization of a hamster oviduct-specific
                                                                                                                                                                                                                                                        EMBL; D32218; BAA06977.1; EMBL; U15048; AAC53584.1;
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Mammalia; Eutheria;
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Malette B., Bleau
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                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Oviduct.
PTM: HIGHLY O-GLYCOSYLATED AND ALSO N-GLYCOSYLATED.
SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
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53:345-354(1995).
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Y., Onuma T., H
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                         ACT_S
                                                                    InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
Pfam; PF00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                       Fisher K.J., Aronson N.N. Jr.; "Cloning and expression of the cDNA sequence glycosidase di-N-acetylchitobiase."; J. Biol. Chem. 267:19607-19616(1992).
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Mammalia; Eutheria; Rodentia;
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                                               SIGNAL
                                                          Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                   Biol. Chem. 267:19607-19616(1992).

FUNCTION: Involved in the degradation of asparagine-linked glycoproteins. Hydrolyze of N-acetyl-beta-D-glucosamine (1-acetylglucosamine chitobiose core from the reducing end of bond, it requires prior cleavage by glycosylasparaginase.

SUBCELLULAR LOCATION: Lysosomal.

SUMILARITY: Belongs to family 18 of glycosyl hydrolases.
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iase precursor (EC 3.2.1.-).
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75.0%;
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Signal; Lysosome; Glycoprotein.
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PROTON DONOR (BY SIMILARITY).
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Sciurognathi; Muridae; Murinae; Rattus.
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InterPro; IPR008967; FN III-like.
InterPro; IPR008961; FN III.
InterPro; IPR001223; Glyco-hydro\_18.
InterPro; IPR001223; Glyco-hydro\_18.
InterPro; IPR001573; Glyco-hydro\_18AS.
Pfam; PF00553; CBM 2; 1.
Pfam; PF007041; fn3; 1.
Pfam; PF007041; Glyco-hydro\_18; 1.

/co\_hydro\_18; 1. Glyco\_hydro\_18;

EMBL; M82804; AAA26720.1; -.
EMBL; M18397; AAA26717.1; -.
PIR; JH0573; JH0573.
HSSP; P07986; 1EXG.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolases).
-!- SIMILARITY: Contains 1 fibronectin type III domain.
-!- SIMILARITY: Contains 1 bacterial-type cellulose-binding
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2; Mismatches
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ACT_SITE
CONFLICT
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-!- INDUCTION: By chitin.
-!- SIMILARITY: Belongs to chitinase class II (family 18
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J. Gen. Microbiol. 139:677-686(1993).
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MEDLINE=93294525; PubMed=8515228;
Fujii T., Miyashita K.;
"Multiple domain structure in a chitinase gene (chiC) of Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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SMART; SM0060; FN3; 1.

SMART; SM00606; Glyco 18; 1.

SMART; SM00606; EF HAND; UNKNOWN_1.

PROSITE; PS00018; EF HAND; UNKNOWN_1.

PROSITE; PS00561; CBD BACTERIAL; 1.

PROSITE; PS01095; CHITINASE_18; 1.

Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal.
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(Rel. 29, Last sequence update)
(Rel. 42, Last annotation update)
precursor (EC 3.2.1.14).
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Pred. No. 0.98;
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CELLULOSE-BINDING.
FIBRONECTIN TYPE-III.
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ProDom; PD000471; Glyco...,

R SMART; SM00637; CBD_II; I.

DR SMART; SM00636; GN3; I.

DR PROSITE; PS00018; EF HAND; UNKNOWN 1.

PROSITE; PS000561; CBD_BACTERIAL; I.

DR PROSITE; PS01095; CHITINASE 18; I.

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PIBRONECTIN TYPE-III.
CATALYTIC.
CATALYTIC.
PROTON DONOR (BY SIMILARITY).
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Search completed: March 22, 2004, 06:53:02 Job time: 1.65203 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Query Match  Best Local Similarity 94.1%; P	SMART; SM00494; ChtBD2; 1.  SMART; SM00636; Glyco 18; 1.  PROSITE, PS01095; CHITTINASE_18; 1  Glycosidase; Hydrolase. SEQUENCE 555 AA; 63238 MW; 0E	GO; GO:0005975; P:carbohydrate metabolism; GO; GO:0006030); P:chitin metabolism; IBA. InterPro; IPR002557; Chitin bind PerA. InterPro; IPR001223; Glyco_hydro_18. InterPro; IPR001273; Glyco_hydro_18AS. Pfam; PF00704; Glyco_hydro_18; 1. ProDom; PD000471; Glyco_hydro_18; 1.	Dermatophagoides farinae (House-dust mite).  Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;  Pyroglyphidae; Dermatophagoides.  NCBI_TaxID=6954;  [1]  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Weber E.R., Hunter S., Stedman K., McCall C.;  "Cloning and Characterization of a 98 kDa Allergen from Dermatophagoides farinae.";  Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  BMSL; AF178772; AAD52672.1;  GO; GO:0008576; C:extracellular; IEA.  GO; GO:0016798; F:chitin binding; IEA.  GO; GO:0016798; F:chitin binding; IEA.  GO; GO:0016798; F:chitin binding; IEA.	Q9U6R7 PRELIMINARY; Q9U6R7; Q9U6R7; C1-MAY-2000 (TrEMBLrel. 13, C 01-MAY-2000 (TrEMBLrel. 13, L 01-OCT-2003 (TrEMBLrel. 25, L 08kPa unm allargen
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R InterPro; IPR003562; FnIII subd. InterPro; IPR003962; FnIII subd. InterPro; IPR003962; FNIII-like. InterPro; IPR003957; FNIII-like. InterPro; IPR003957; FNIII-like. R InterPro; IPR001223; Glyco hydro 18. InterPro; IPR001273; Glyco hydro 18. R InterPro; IPR001579; Glyco-hydro_18AS. R InterPro; IPR001579; Glyco-hydro_18AS. R Ffam; PF00241; fn3; 1. R Ffam; PF00241; fn3; 1. R Ffam; PF00704; Glyco-hydro_18; 1. R Ffam; PF00704; Glyco-hydro_18; 2. R Ffam; PF00704; Glyco-hydro_18; 2. R FANDON; DD0004071; Glyco-hydro_18; 2. R SMART; SM000495; ChtBD3; 1. R SMART; SM000495; ChtBD3; 1. R SMART; SM000495; ChtBD3; 1. R SMART; SM00060; FN3; 1. R SMART; SM000060; FN3; 1. R SMART; SM00000; FN3; 1. R SMART; SM00000; FN3; 1. R SMART; SM00000; FN3; 1. R SMART; SM000000; FN3; 1. R SMART; SM00000000; FN3; 1. R SMAR
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                                                                                  SEQUENCE FROM N.A. MEDLINE=20403594; PubMed=10949318;
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                                             Woytowich A.E., Selvaraj G., Khachatourians G.G.;
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SUBMITTED (JUL-2001) to the EMBL/GenBank/DDBJ databas EMBL; AF99871; AAN03597.1; -.

RO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0016787; F:hydrolase activity, hydrolyzing O-9

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:001579; F:hydrolase activity; IEA.

GO; GO:001579; F:carbohydrate metabolism; IEA.

InterPro; IPR001579; Glyco_hydro_18

InterPro; IPR00123; Glyco_hydro_18

InterPro; IPR00123; Glyco_hydro_18AS.

Pfam; PF00704, Glyco_hydro_18; 1.

R Pfam; PF00704, Glyco_hydro_18; 1.

R PFADDOM; ED000471; Glyco_hydro_18; 1.

R PFADDOM; ED000471; Glyco_hydro_18; 1.

R PROSITE; EN00636; Glyco_19; 1.

R PROSITE; PS01095; ChrED3; 1.

R PROSITE; PS01095; CHRED3; 1.

R PROSITE; PS01095; Glyco_18; 1.

R PROSITE; PS01095; Glyco_18; 1.

R PROSITE; PS01095; Glyco_18; 1.
GO; GO:000552; F:AIP binding; IEA.
GO; GO:0004553; F:hydrolase activity, hydroly;
GO; GO:0004811; F:tRAN ligase activity; IEA.
GO; GO:0006418; P:tRAN ligase activity; IEA.
GO; GO:0006418; P:tRAN ligase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEI.
InterPro; IPR001919; Bac celose-bind.
InterPro; IPR008957; FN III-like.
InterPro; IPR00123; Glyco_hydro_18.
InterPro; IPR00123; Glyco_hydro_18AS.
InterPro; IPR00123; Glyco_hydro_18AS.
InterPro; IPR001579; Glyco_hydro_18AS.
InterPro; IPR001573; Glyco_hydro_18; 1.
Pfam; PF00553; CBM 2; 1.
Pfam; PF00704; Glyco_hydro_18; 1.
Pfam; PF00704; Glyco_hydro_18; 1.
PFAMP; SM00637; CBD_II; 1.
SMART; SM00637; CBD_II; 1.
SMART; SM00636; Glyco_18; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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Q9FAC8;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. -:- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOW EMBL; AB041932; BAB16891.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus cereus.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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J. Biotechnol.
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"Chitinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Similarity 84.6%;
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Last annotation updat
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Pred. No. 0.
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databases.
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R GO; GO:0005524; F:ATP binding; IEA,
GO; GO:000453; F:hydrolase activity, hydrolyzing (
R GO; GO:000453; F:hydrolase activity; IEA,
R GO; GO:0016787; F:hydrolase activity; IEA,
JR GO; GO:0004812; F:tRNA ligase activity; IEA,
JR GO; GO:0006418; F:amino acid activation; IEA,
JR GO; GO:0005975; P:carbohydrate metabolism; IEA,
JR GO; GO:0005975; P:carbohydrate metabolism; IEA,
JR InterPro; IPR001919; Bac celose-bind.
DR InterPro; IPR001919; Bar celose-bind.
DR InterPro; IPR008965; Cellul bind.
DR InterPro; IPR008965; PM III-like.
DR InterPro; IPR008967; FM III-like.
InterPro; IPR00897; FM III-like.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001279; Glyco_hydro_18AS.
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Best Local S
Matches 11
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Best Local (
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SMART; S
                                                                                                                          Q81Z87;
01-JUN-2003
01-JUN-2003
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Chitinase B.
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SMART; SM00636; Glyco 18; 1.
PROSITE; PS00178; AA TRNA LIGASE
PROSITE; PS01095; CHITINASE 18;
PROSITE; PS01095; CHITINASE 18;
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Pfam; PF00704; Glyco hydro 18; 1.

ProDom; PD000471; Glyco hydro_18;

SMART; SM00637; CBD_II; 1.

SMART; SM00060; FN3; 1.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY074882; ALT11886.2; -
GO; GO:0005524; F:ATP binding; IEA.
                                                                                                                                                                                                                                                                                         Q81Z87
   BA0385.
Bacilla anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales;
NCBI_TaxID=198094;
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Bacteria; Firmicutes; E
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TRNA LIGASE I; 1.
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91.7%;
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                                                                                                                                                               24,
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, Last sequence up
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Pred. No.
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Pred. No. 0.
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                                    Bacillaceae; Bacillus
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0.023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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Q811F9;
01-JUN-2003 (TrEMBLrel. 24, Cr
01-JUN-2003 (TrEMBLrel. 24, La
01-OCT-2003 (TrEMBLrel. 25, La
Endochitinase (EC 3.2.1.14).
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SEQUENCE FROM N.A.

MEDLINE=22608415; PubMed=12721630;

MEDLINE=22608415; PubMed=12721630;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapid

Kapatral V., Bhattacharyya A., Larsen N., D'Souza M., Walunas

Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas

Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.

Overbeek R., Kyrpides N.;

Lapidus

Bacteria; Firmicutes; Bacillus cereus (strain

in ATCC 14579 / DSM 31). Bacillales; Bacillaceas

Bacillaceae;

Bacillus

Created)
Last sequence update)
Last annotation updat

update)

PRT;

674

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NCBI\_TaxID=226900;

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Matches
                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                 Pfam; PF00553; CBM 2; 1.
Pfam; PF00041; fn3; 1.
Pfam; PF000704; Glyco hydro 18; 1.
Pfam; PF0000471; Glyco hydro 18; 2.
SMART; SM00637; CBD II; 1.
SMART; SM0066; FN3; 1.
SMART; SM00666; Glyco 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001919; Bac_celose-bind.
InterPro; IPR008965; Cellul_bind.
InterPro; IPR008961; FN III.
InterPro; IPR008967; FN III-like.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                PROSITE;
PROSITE;
Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Melson K.B., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Holtzapple E.K., Okstad O.A., Holtzapple E.K., Okstad O.A., Dodson R.J., Brinkac L.M., Gwinn M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Senton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S. Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'The genome sequence of Bacillus anthracis closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22608414; PubMed=12721629;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005524; F:ATP binding; IEA.
GO:0004533; F:hydrolase activity; hydrolyzi
GO:0016787; F:hydrolase activity; IEA.
GO:0004812; F:tRNA ligase activity; IEA.
GO:0006418; P:amino acid activation; IEA.
GO:0005975; P:carbohydrate metabolism; IEA.
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                                                                                                                                                                  Similarity
                                                                                                  DKLVMGVPFYGR 12
                                                                                                                                                                                                                                                    protecme
                                                                                                                                                                                                                                                                     PS00178; AA_TRNA_LIGASE_I; 1.
PS01095; CHITINASE_18; 1.
                                                             DKLVLGVPFYGR
                                                                                                                                                                                                                                  674 AA;
                                                                                                                                            Conservative
                                                                                                                                                                                                                                  74161 MW;
                                                                                                                                                                                                                                                                                             TRNA
                                                                                                                                                                  74.7%;
91.7%;
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                                                                                                                                                                  Score 62;
Pred. No.
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RESULT 8

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AC Q93A

AC Q9A

AC Q
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Q93AD3;
Q93AD2;
Q1-DEC-2001 (TrEMBLrel. 19, Cr
P 01-DEC-2001 (TrEMBLrel. 19, Le
P 01-CT-2003 (TrEMBLrel. 25, Le
P 01-CT-2003 (TrEMBLrel. 25, Le
P 01-CT-101486 (EC 3.2.1.14).
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R Pfam; PF007041; fin3; 1.

R Pfam; PF00704; Glyco_bydro_18; 1.

R ProDom; PD000471; Glyco_bydro_18; 2.

R SMART; SM00637; CBD_II; 1.

R SMART; SM00636; FN3; 1.

R SMART; SM00636; Glyco_18; 1.

R PROSITE; PS00178; AA TRNA LIGASE I; 1.

R PROSITE; PS01095; CHTTINASE 18; 1.

R PROSITE; PS01095; CHTTINASE 18; 1.

Glycosidase; Hydrolase; Complete proteome.

W Glycosidase; Hydrolase; Complete Proteome.
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Best Local :
                                                                                                                                                         III SINILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LEMBL; AF424979; AAL17867.1; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005843; F:endochitinase activity; IEA.

GO; GO:0004812; F:tRNA ligase activity; IEA.

GO; GO:0006418; P:amino acid activation; IEA.

GO; GO:0006418; P:amino acid activation; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR001919; Bac celose-bind.

InterPro; IPR001919; Bac celose-bind.

InterPro; IPR003961; FN_III.

InterPro; IPR003961; FN_III.

InterPro; IPR001223; GIJVco_hydro_18AS.

InterPro; IPR001579; Glyco_hydro_18AS.

InterPro; IPR001579; Glyco_hydro_18AS.

InterPro; IPR001412; tRNA-Bynt_I.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008843; F:endochitinase activity; IEA.
GO; GO:0008843; F:endochitinase activity; IEA.
GO; GO:0004812; F:tRNA ligase activity; IEA.
GO; GO:0006418; P:amino acid activation; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001919; Bac celose-bind.
InterPro; IPR001919; Bac celose-bind.
InterPro; IPR001965; Cellul bind.
InterPro; IPR003965; FN_III-
InterPro; IPR003967; FN_III-like.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001579; Glyco_hydro_18AS.
InterPro; IPR001579; Glyco_hydro_18AS.
InterPro; IPR001579; Glyco_hydro_18AS.
InterPro; IPR001579; Glyco_hydro_18AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of a chitinase gene from a Mexican strain of Buthuringiensis.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales,
NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Barboza-Corona E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Ba
Bacillus anthracis.";
Nature 423:87-91(2003)
                                          Pfam; PF00553; CBM
Pfam; PF00041; fn3;
Pfam; PF00704; Glyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330
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    /co_hydro_18; 1.
Glyco_hydro_18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Velazquez-Robledo R.,
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91.7%;
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Last annotation updat
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Pred. No. 0.02
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o R., Nieto-Mazzoco E.;
Mexican strain of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and comparative
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RESULT Q8KNY3

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                                            Query Match
Best Local S
Matches 11
                                                                                                                                                                                               EMBL; AP416570; AAM48520.1; ...

GC; GO:0008524; F:ATP binding; IEA.

GC; GO:000843; F:endochitinase activity; IEA.

GC; GO:0008412; F:tRNA ligase activity; IEA.

GC; GO:0006418; P:amino acid activation; IEA.

GC; GO:0006918; P:amino acid activation; IEA.

GC; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR001919; Bac celose-bind.

InterPro; IPR001919; Bac celose-bind.

InterPro; IPR008965; CelTul_bind.

InterPro; IPR008965; FN III-like.

InterPro; IPR00123; Glyco_hydro_18.

InterPro; IPR00123; Glyco_hydro_18AS.

InterPro; IPR001412; tRAA-Bynt_I.

R Ffam; PF00553; CBM 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08KVU8;
01-0CT-2002
01-0CT-2002
01-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00637; CBD_II; 1.

SMART; SM00060; FN3; 1.

SMART; SM00636; Glyco_18; 1.

PROSITE; PS00178; AA_TENA_LIGASE_I;

PROSITE; PS01095; CHITINASE_18; 1.

Glycosidase; Hydrolase.
                                                                                                                            Pfam; PF00704; Glyco hydro 18; 1.
ProDom; PD000471; Glyco hydro 18;
SMART; SM00637; CBD II; 1.
SMART; SM00060; FM3; II;
SMART; SM00036; Glyco 18; 1.
PROSITE; PS00178; AA TRNA LIGASE I
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus cereus.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                    Hydrolase;
                                                                                                               PROSITE; PS00178; AA TRNA LIGASI
PROSITE; PS01095; CHITINASE 18;
                                                                                                                                                                                                                                                                                                                                                                                                         cereus."
                                                                                                                                                                                                                                                                                                                                                                                                                   Chen C.-Y., Huang C.-J., Wang T.-K.; "Cloning of a chitinase gene from an antagonistic
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=28-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chitinase CW
344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 DKLVLGVPFYGR 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DKLVMGVPFYGR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                        Similarity
DKLVLGVPFYGR
                      DKLVMGVPFYGR 12
                                                                                           Glycosidase.
688 AA; 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (TrEMBLrel. 22,
2 (TrEMBLrel. 22,
3 (TrEMBLrel. 25,
TW (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 AA; 74469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                             Conservative
                                                        74.78;
                                                                                           75859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.78;
91.78;
                                                                                                                   TENA LIGASE I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                             Score 62; DB 2;
Pred. No. 0.024;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A7B7DAFB621516C9 CRC64;
                                                                                           69AB97F728A292E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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IEA.
                                                                   DB 2;
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                                                                                            CRC64;
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                                              Indels
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RESULT 11
Q8KRQ5
ID Q8KRQ
AC Q8KRQ
AC Q8KRQ
AC Q8KRQ
AC Q8KRQ
DT 01-OC
DT 0
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2002) to the EMBI/GenBank/DDBJ date
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LI
EMBL; AN129671; AAM94024.1; -

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004553; F:hydrolase activity; IEA.

GO; GO:0004812; F:tRNA ligase activity; IEA.

GO; GO:0004812; F:tRNA ligase activity; IEA.

GO; GO:0006418; P:amino acid activation; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR001919; Bac celose-bind.

InterPro; IPR001957; FN_III-like.

InterPro; IPR001223; Glyco-hydro-18.

InterPro; IPR00123; Glyco-hydro-18AS.

InterPro; IPR001412; tRNA-synt_I.

Pfam: PF00553; CBM 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00553; CBM 2; 1.

Pfam; PF00541; f135 1.

Pfam; PF00704; Gly50_hydro_18; 1.

Pfam; PF00704; Gly50_hydro_18; 2.

PF0Dom; PD000471; Gly50_hydro_18; 2.

SMART; SM00637; CBD_II; 1.

SMART; SM00636; PN3; 1.

SMART; SM00636; Gly50_18; 1.

SMART; SM00636; Gly50_18; 1.

PROSITE; PS01095; CHITINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                            Q8KRQ5
Q8KRQ5;
Q1-OCT-2002
01-OCT-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002
01-OCT-2002
01-OCT-2003
Chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS
Hydrolase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8KNY3;
         SEQUENCE FROM N.A.

Zhong W.F., Yan W.Z., Jiang L.H., Cai P.Z.;

Zhong M.F., Yan W.Z., Jiang L.H., Cai P.Z.;

"Cloning and sequence analysis of chitinase gene from
thuringiensis.";

submitted (UUL-2002) to the EMBL/GenBank/DDBJ databas
-!-SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE
EMBL; AF526379; AAM88400.1; -.

GO; GO:0005524; F:ATP binding; IEA.
                                                                                                                                                                                                      NCBI_TaxID=1430;
[1]
                                                                                                                                                                                                                                                  Bacillus thuringiensis
Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis (subsp. sotto).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=29340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thuringiensis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Cloning and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKLVMGVPFYGR
                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     688 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W.Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiang L.H.,
analysis of
                                                                                                                                                                                                                                                  s (subsp. israelensis).
Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355
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Last sequence update)
Last annotation update)
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Pred. No.
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chitinase
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1.024;
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                                                                                                                                  from Bacillus
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                                                               DOMAINS
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Q84FN2
                   AC CONTRACTOR AND ACTOR ACTOR AND ACTOR AC
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Best Local S
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kurstaki.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O84FN2;
O84FN2;
O1-JUN-2003
O1-JUN-2003
O1-OCT-2003
PRODOM; FLOOT:
SMART; SM00637; CBD_II; 1.
SMART; SM0066; FN3; 1.
SMART; SM00636; Glyco_18; 1.
SMART; SM00636; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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GO; GO:0004553; F:hydrolase activity, hydrolyzing
GO; GO:0004812; F:hydrolase activity; IEA.
GO; GO:0004812; F:trNA ligase activity; IEA.
GO; GO:0006418; F:trNA ligase activity; IEA.
GO; GO:0006418; F:amino acid activation; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
R GO; GO:0005975; P:carbohydrate metabolism; IEA.
R InterPro; IPR008965; Cellul bind.
R InterPro; IPR008965; FN_III-
INTERPRO; IPR008957; FN_III-
R InterPro; IPR008957; FN_III-
R InterPro; IPR001273; Glyco_hydro_18.
R InterPro; IPR001579; Glyco_hydro_18AS.
R InterPro; IPR001579; Glyco_hydro_18AS.
R InterPro; IPR001579; Glyco_hydro_18; 1.
R Pfam; PF00704; Glyco_hydro_18; 1.
R Pfam; PF00704; Glyco_hydro_18; 2.
R Pfam; PF00704; Glyco_hydro_18; 2.
R Pfam; PF00704; Glyco_hydro_18; 1.
R PfAMPT; SM00636; Glyco_hydro_18; 1.
R SMART; SM00636; Glyco_18; 1.
R PROSITE; PS01095; CHITINASE_18; 1.
R PROSITE; PS01095; CHITINASE_18; 1.
R PROSITE; PS01095; CHITINASE_18; 1.
EMBL; AY189740; AAC34713.1; -...

GC; GC:0005524; F:ATP binding; IEA.

GC; GC:0004553; F:hydrolase activity, hydrolyzing O-g

GC; GC:0016787; F:hydrolase activity; IEA.

GC; GC:0016787; F:hydrolase activity; IEA.

GC; GC:0004812; F:tRNA ligase activity; IEA.

GC; GC:0005975; P:carbohydrate metabolism; IEA.

R GC; GC:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR001919; Bac_celose-bind.

R InterPro; IPR001923; GIVCO_hydro_18.

R InterPro; IPR00123; GIVCO_hydro_18AS.

R InterPro; IPR001471; tRNA-synt_I.

R Ffam; PF00553; CBM_2; 1.

R Pfam; PF000704, GIVCO_hydro_18; 2.

R SMART; SM00637; CBD II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis (subsp. kurstaki).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
MCBI_TaxID=29339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKLVMGVPFYGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L.H., Yan W.Z., Cai P.Z., Xiang Y.W., 2 of chitinase gene cloned from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75788 MW; 0FC0DCF71760D1C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         889
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s thuringiensis
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RESULT
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R PDB; 1E15; 18-AUG-00.
PDB; 1E6N; 22-JUN-01.
PDB; 1E6R; 22-JUN-01.
PDB; 1E6R; 22-JUN-01.
PDB; 1E6R; 22-JUN-01.
PDB; 1E6R; 22-JUN-01.
R PDB; 1E6R; 22-JUN-01.
PDB; 1E6R; 22-JUN-01.
R PDB; 1GF; 31-OCT-02.
R PDB; 1GF; 31-OCT-02.
R CO; GO:0005576; C:extracellular; IEA.
RCO; GO:0005276; F:carbohydrate binding; IEA.
RCO; GO:0005276; F:carbohydrate metabolism; IEA.
RCO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .;
RCO; GO:0005975; P:carbohydrate metabolism; IEA.
R GO; GO:0005975; P:carbohydrate metabolism; IEA.
R FAGN; PR001273; Glyco_hydro_18.
R FAGN; PF00339; CBM_5_12; 1.
R Pf00m; PP00349; CBM_5_12; 1.
R Pf00m; PP000471; Glyco_hydro_18; 1.
R PRODM; PD000471; Glyco_hydro_18; 1.
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Best Local S
Matches 11
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Best Local
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Q59929;
Q59929;
01-NOV-1996
01-NOV-1996
01-OCT-2003
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Q54276;
Q1-NOV-1996
Q1-NOV-1996
Q1-OCT-2003
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Glycosidase; Hydrolase.
SEQUENCE 499 AA; 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   periplasm without processing.";
Microbiology 141:123-131(1995).
EMBL; Z36295; CAA85292.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=95202070; PubMed=7894703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serratia marcescens.
Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae;
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E; PS01095; CHITINASE_18; 1.
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                                                                                                                                                             Similarity 91.
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                                                                                                              KIVMGVPFYGRA 295
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91.7%;
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Pred. No. 0.02,
1; Mismatches
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Last annotation update)
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                                                                                                                                                                                       Score 61;
                                                   PRT;
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F9D552062575AAB4 CRC64;
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sequence update) annotation update)
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0.024;
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is exported to
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Q8MSI4
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GO; GO:0030246; F:carbohydrate binding; IEA.
GO; GO:0030246; F:carbohydrate binding; IEA.
GO; GO:000843; F:endochitinase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEI
InterPro; IPR00123; Glyco_hydro_18.
InterPro; IPR001233; Glyco_hydro_18.
Pfam; PP002839; CBM_5_12; 1.
Pfam; PP00704; Glyco_hydro_18; 1.
ProDom; PD000471; Glyco_hydro_18; 1.
SMART; SM00349; ChnED3; 1.
SMART; SM00349; ChnED3; 1.
SMART; SM00349; ChnED3; 1.
Glycosidase; Hydrolase; Signal.
SIGNAL
1
24
POTENTIAL.
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Best Local
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EMBL; AY118784; AAM50644.1;
FlyBase; FBgn0034580; CG9357.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000861; F:chittn binding; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0006030; P:chittn metabolism; IEA.
GO; GO:0006457; P:metabolism; IEA.
GO; GO:0006457; P:protein folding; IEA.
GO; GO:0006457; P:protein folding; IEA.
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Q8MSI4;
01-OCT-2002
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-Berkeley;

STRAIN-Berkeley;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson of Stapleton M., Chavez C., Dorsett V., Dreenek D., Farfan D., Fi George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Li Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubi Celniker S.;

Celniker S.;

Celniker S.;

Colliner S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins.
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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FEMS Microbiol. Lett. 151:197-204(1997).
EMBL, L38484, AAC37122.1;
HSSP; P07254; 1CTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002
01-OCT-2003
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Lee S.Y., Cho M.J.;
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/., Kim C.Y., Cheong
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58107 MW;
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CHITINASE.
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Pred. No. 0.027;
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era; Muscomorpha;
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                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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protein search, using sw model
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length: 2000000000
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83
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Minimum Match
Maximum Match
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geneseqp2000s:*
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02-SEP-1998;
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Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen pro -map) composition. The HWM-map composition was isolated from a D homogenate by gel filtration, with each fraction being analysed presence of proteins that bound to IgE present in mite-allergic

protein (HWM D. farinae ed for the ic dog

Claim 3; Page 70; 154pp; English.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

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Query Match
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Matches 17
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                  The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein is useful for reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig) or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines
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Der HMW-map protein, useful
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allergen hypersensitivity. Sequences AAU96314-AAU96342
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2.8e-08;
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13-MAY-1998;
02-SEP-1998;
          This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-490, the mature form of pDerp98-509, PDerp98-490 has a molecular weight of 98 kD, comprising 490 amino acids, and has a high degree of homology with the D. farinae mature 98 kD allergeen, maps (AAY52525). Nucleic acid molecules encoding PDerp98-490 were isolated from a D. pteronyssius cDNA library by hybridisation with a probe encoding the D. farinae high molecular weight map (HMW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergeis via a skin test. The proteins and
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22-FEB-2000
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                                                                                                                                                                                                              Claim 3; Page 147-149; 154pp; English
                                                                                                                                                                                                                                          Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
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                                                     The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-protein acceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. An interpretation is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig) or Der HMW-map protein activity associated with a clisease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 or represent Der HMW-map polypeptides of the invention
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Best Local :
   Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mite allergenic protein isolated from Dermatophagoides,
Der HYW-map protein, useful as a vaccine for treating mite a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 144-146; 161pp; English.
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2e-06;
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Score 80; DB Pred. No. 2e-0 0; Mismatches

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Indels

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                                                           This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD, cc comprising 509 amino acids, and has a high degree of homology with the D farinae 98 kD allergen, maps (AAVS2523). Nucleic acid molecules encoding PDerp98-509 were isolated from a D. pteronyssius cDNA library by PDerp98-509 were isolated from a D. pteronyssius cDNA library by CC hybridisation with a probe encoding the D. farinae high molecular weight map (HWW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allerges via a skin cest. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as topose to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins. (Updated con 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 134-136; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
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                                                                                                                                                                                                                                                                                       Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANJ96314-AAJ96342 represent Der HMW-map polypeptides of the invention
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                                                                                                                                                                                                                                      Sequence 509
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Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mccall CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1mmunocomplex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 134-136; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-351888/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000; 2000US-00662293
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                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273
273
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                                                                                                                    16;
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKLVMGVPFYGRAWSIE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKLVMGVPFYGRAXSIE
                                                       DKLVMGVPFYGRAXSIE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide #24
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.4%;
94.1%;
                                                                                                                                             96.4%;
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                                                                                                                 0;
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Pred. No. 2.1e-06;
                                                                                                                                             Score 80; DB 5; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 509;
                                                                                                                                                                     Length 509;
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                                                                                                                    Indels
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                                                                                                                 Gaps
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RESULT 7

RESULT 8
AAY52525
ID AAY5
XX
AC AAY5
AC AAY5
XX
AC AAY5
XX
AC Hous
XX
DT 22-F
XX
DE Hous
XX
Mite

AAY52525 standard; protein; 536

B

0

22-FEB-2000 AAY52525

(first entry) Θ̈.

House dust mite

Mite allergen protein; map; high molecular weight;

farinae) mite allergen

protein

HMW-map; allergy; (map) PDerf98-536

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AAU96338

IID AAU96

XX XX IID DET IS-U
XX DET IS-U
XX
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                                                                Ś
                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated mite allergenic protein of CD Dermatophagoides, designated Der HMW-map protein, and its related nucleic CD acid. The Der HMW-map protein is useful for eliciting an immune response CD against Der HMW-map protein. The protein or a reagent comprising a non-protein account spitope is useful for identifying an animal (e.g., dog, CD act) susceptible to or having an allergic response to a mite. A CD therapeutic composition is useful for desensitising a host animal to an CD allergic response to a mite. The DNA and protein can be used in the CD detection of anti-Der HMW-map antibodies in animal fluids, and inhibition CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies that bind to Der HMW-map are useful for inhibiting CD disease. Antibodies disease to mite allergens, and as vaccines CD against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
                                                                                                                                            Query Match
Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU96338;
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                                                                                                                                                                                                                                                                                        Sequence 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2001; 2001WO-US028730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Der HMW-map polypeptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mite allergenic protein isolated from Dermatophagoides, designa HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-351888/38
)B; ABK69583.
273
                                                                                                                                                16;
                                                                                                                                                                              Similarity
DKLVMGVPFYGRAWSIE 289
                                                                    DKLVMGVPFYGRAXSIE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 139-141; 161pp; English.
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                A
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                                                                                                                                                                              96.4%;
                                                                                                                                            0
                                                                                                                                            Score 80; DB
Pred. No. 2.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R
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                                                                                                                                                                              2.1e-06;
                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                Length 509;
                                                                                                                                                0;
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RESULT 9
AAU96329
ID AAU96329
XX AAU9
XX AAU9
XX Der
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (map) PDerf98-536, the mature form of pDerf98-555 (AAY52523). PDerf98-536
Chas a molecular weight of 98 kD, comprising 536 amino acids, and is a
component of the Dermatophagoides farinae high molecular weight mite
component of the Dermatophagoides farinae high molecular weight mite
component of the Dermatophagoides farinae high molecular weight mite
component of the Dermatophagoides farinae high molecular weight mite
composition of the presence of proteins that bound to IgE
present in mite-allergic dog antisera. Mite allergenic proteins and
peptides, and nucleic acids encoding them, may be used in therapeutic
compositions to modify an animal's hypersensitivity reaction to mite
compositions to modify an animal's hypersensitivity reaction to mite
compositions to modify an animal's hypersensitivity reaction to mite
compositions to modify an animal's hypersensitivity reaction to mite
composition and peptides and work or
composition as kin test. The proteins of ragments may also be used to diagnose
composition to mite
composition as which have a variety of potential uses. For example,
composition to mite allergens to passively immunise animals against dust
mite hypersensitivity, as positive controls in test kits and as tools to
control to mite and the proteins of proteins.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                   Matches
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13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-536, the mature form of PDerf98-55 (AAY52523). PDerf98-5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-052700/04.
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                                                                                                                                                                                  AAU96329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA
                                                        mite
                                                                                                                                                                                                                   AAU96329 standard;
 Dermatophagoides farinae
                                                       Der HMW-map; American house dust mite; antiallergic; mite allergenic protein; immunoglobulin E; hypersens:
                                                                                                        Der HMW-map polypeptide #16.
                                                                                                                                               15-JUL-2002
                                  immunocomplex formation
                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ38579,
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                             DKLVMGVPFYGRAWSIE 270
                                                                                                                                                                                                                                                                                                                                 DKLVMGVPFYGRAXSIE
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125-127; 154pp; English.
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98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ38580
                                                                                                                                                                                                                   protein; 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ws
                                                                                                                                                                                                                                                                                                                                                                                                96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weber
                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                  Score 80;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
2.2e-06;
                                                     hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 536;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                     IgE;
                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          feline;
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WO9954349-A2

Protein

"Mature PDerf98-555"

Peptide

Location/Qualifiers 'note= "Signal peptide"

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AAY5233
ID AAY523
XX AAY52
XX AAY52
XX AAY52
XX AAY52
XX AAY52
DT 22-FE
XX Mite
DE House
XX Mite
KW house
XX Mite
XX Derma
XX Canin
XX Canin
XX Pri Pepti
FT Prote
FT Prote
FT YX WO995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic caid. The Der HMW-map protein is useful for eliciting an immune response cagainst Der HMW-map protein. The protein or a reagent comprising a non-compressing expectation or a reagent comprising a non-compression or having an allergic response to a mite. A composition is useful for desensitising a host animal to an expectation composition is useful for desensitising a host animal to an expectation of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a composition start bard to Der HMW-map are useful for inhibition of immunoglobulin (Ig) E or Der HMW-map are useful for inhibition complexes. Antibodies that bind to Der HMW-map are useful for inhibition complexes antibodies that bind to Der HMW-map are useful for inhibiting compositions to IgE, to prevent immunocomplex formation, thus cagainst mite allergen hypersensitivity. Sequences AAU96314-AAU96342 corepresent Der HMW-map polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 125-127; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mite allergenic protein isolated from 
Der HMW-map protein, useful as a vaccine i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccall CA, Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200222807-A2
                                                                                                                                                                                           Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fel
                                                                                                                                                                                                                                                                                                                                                              AAY52523 standard; protein; 555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated mite allergenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                                                                               22-FEB-2000
                                                                                                                                                                                                                                                                                                                                 AAY52523
                                                                                                                                               Dermatophagoides farinae
                                                                                                                                                                                                                                                               House dust mite (D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-351888/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 DKLVMGVPFYGRAWSIE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK69575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKLVMGVPFYGRAXSIE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                               farinae) mite allergen protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.4%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; 1
2.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dermatophagoides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating
                                                                                                                                                                                             diagnosis; human; feline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 536;
                                                                                                                                                                                                                                                               (map)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mite
                                                                                                                                                                                                                                                                  PDerf98-555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel
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13-MAY-1998;
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           14-SEP-2000; 2000US-00662293
                                        14-SEP-2001;
                                                                                                WO200222807-A2
                                                                                                                      Dermatophagoides farinae
                                                                                                                                                                      mite
                                                                                                                                                                                  Der HMW-map;
                                                                                                                                                                                                             Der HMW-map polypeptide #14
                                                                                                                                                                                                                                            15-JUL-2002
                                                                                                                                                                                                                                                                                                 AAU96327 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 555
                                                                                                                                                       immunocomplex
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                       allergenic protein; nocomplex formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                       DKLVMGVPFYGRAXSIE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from a mixture of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                        2001WO-US028730.
                                                                                                                                                                   American house dust mite; antiallergic; mite; IgE; nic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP.
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00062013.
98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ38576, AAZ38577, AAZ38578
                                                                                                                                                                                                                                                                                                                                                                                                                                              96.4%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            t Dermatophagoides nucleic acid polypeptides hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                          289
                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 80; DB 3; 1
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    景
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 12
AAU96328
ID AAU966
XX
AC AAU96
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DT 15-JT
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DE Der
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DE Mmite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reducing hypersensitivity responses to mite allergens, and as vacciagainst mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 114-116; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Der HMW-map; American house dust mite; antiallergic; mite; I mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Der HMW-map polypeptide #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2002
                                                                                                                                                                      Mccall CA, Hunter SW,
                                                                                                                                                                                                                                                                                  14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                            14-SEP-2001; 2001WO-US028730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200222807-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dermatophagoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunocomplex formation.
                                                                                                                                                                                                                             (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                    2002-351888/38
DB; ABK69573.
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16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKLVMGVPFYGRAXSIE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKLVMGVPFYGRAWSIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 555
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                                                                                                                                                                         Weber ER
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; I
2.3e-06;
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New mite allergenic protein isolated from Dermatophagoides, Der HMW-map protein, useful as a vaccine for treating mite a

allergy.

designated

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RESULT 13
ABB64366
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Best Local S
Matches 16
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                    New isolated nucleic a
genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide,
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                                                                                                                                                                                   Disclosure; SEQ ID NO 19890; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL08469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to Ig3, to prevent immunocomplex formation, thus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKLVMGVPFYGRAWSIE
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a and
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94.1%;
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                                                                                                                                                                                                                                                                    detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers
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                                                                                                                                                                                      English.
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AAE28199 ID AAE2 XX RESULT 15

AAE28199

standard; protein;

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NKLVVGVÞFYGRSFTL

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1 DKLVMGVPFYGRAXSI 16

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RESULT 14
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ID AAE28
XX AAE28
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XX Flea;
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Best Local (
                                                   Query Match
                                                                                                                                                           The present invention relates to flea chitinase (CHT) proteins and their corresponding polynucleotides. Sequences of the invention are useful for protecting an animal from flea infestation or to reduce flea infestation in an animal susceptible to flea infestation. They are also used in gene therapy. The present sequence is flea chitinase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences (ABL01840-ABL16175) and the encoded proteins (ABS7737-AB372072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                             Sequence 489 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated flea chitinase nucleic acid useful for protecting animal from flea infestation or to reduce flea infestation in an susceptible to flea infestation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE28202 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD45161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-2000; 2000US-00545814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flea chitinase protein, PCfCHT489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-DEC-2002
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                                                                                                                                                                                                                                                                                                                                     Example 1; Col 81-84; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Becher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6416977-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HESK-) HESKA
                               Local
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l Similarity
10; Conserv
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9; Conserv
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  Conservative
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                       71.1%;
62.5%;
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Pred. No.
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Pred. No.
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                                                   DB 5;
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Search completed: March 22, 2004, 06:51:42
Job time : 6.16898 secs
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                                                                                                              Query Match 71.1%; Score 59; DB 5; Length 559; Best Local Similarity 62.5%; Pred. No. 0.023; Matches 10; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                The present invention relates to flea chitinase (CHT) proteins and their corresponding polynucleotides. Sequences of the invention are useful for protecting an animal from flea infestation or to reduce flea infestation in an animal susceptible to flea infestation. They are also used in gene therapy. The present sequence is flea mature chitinase protein
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-634733/68.
N-PSDB; AAD45152.
                                                                                                                                                                          Sequence 559 AA;
                                                                                                                                                                                                                                                                                      Claim 4; Col 69-72; 50pp; English.
                                                                                                                                                                                                                                                                                                                  Novel isolated flea chitinase nucleic acid useful for protecting an animal from flea infestation or to reduce flea infestation in an animal susceptible to flea infestation.
                                                                                                                                                                                                                                                                                                                                                                                                                      Becher AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-2000; 2000US-00545814.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ctenocephalides felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flea; chitinase; enzyme; flea infestation; gene therapy; insecticide; CHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flea PCfCHT583 mature chitinase protein, PCfCHT559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE28199;
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                                                        1 DKLVMGVPFYGRAXSI 16 :|||:||||||: :: 257
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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                                                               and is derived by analysis of the total score distribution.
                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-662-293-10
83
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1265.926 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/US09B PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C PUBCOMB.pep:*
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SUMMARIES
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63.9	66.3	66.3	66.3	66.3	74.7	96.4	96.4	96.4	96.4	96.4	96.4	97.6	Query Match
392	599	572	449	366	428	555	555	536	509	509	490	17	Length
ם ה	15	15	15	12	<u>1</u> 5	14	14	14	14	14	14	14	BG
US-10-369-493-19361	US-10-369-493-17162	US-10-369-493-18585	US-10-369-493-3308	US-10-424-599-209667	US-10-369-493-16644	US-10-218-743-18	US-10-218-743-15	US-10-218-743-21	US-10-218-743-38	US-10-218-743-35	US-10-218-743-41	US-10-218-743-10	ID
Sequence 19361, A	Sequence 17162, A	Sequence 18585, A	Sequence 3308, Ap	Sequence 209667,	Sequence 16644, A	18,	•	~	Sequence 38, Appl	35,	41,	10,	Description
	53 63.9 392 15 US-10-369-493-19361 Sequence	55 66.3 599 15 US-10-369-493-17162 Sequence 53 63.3 929 15 US-10-369-493-19361 Sequence 51 61 67 67 67 67 67 67 67 67 67 67 67 67 67	55 66.3 572 15 US-10-369-493-18585 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence 53 63.9 392 15 US-10-369-493-19361 Sequence 53 63.4 678 15 US-10-285-027-623	66.3 449 15 US-10-369-493-3308 Sequence 66.3 572 15 US-10-369-493-19162 Sequence 66.3 599 15 US-10-369-493-17162 Sequence 63.9 392 15 US-10-369-493-19361 Sequence 63.9 392 15 US-10-369-493-19361 Sequence	55 66.3 366 12 US-10-424-599-209667 Sequence 55 66.3 449 15 US-10-369-493-3088 Sequence 55 66.3 572 15 US-10-369-493-18585 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence 53 63.9 352 15 US-10-369-493-17365 Sequence	62 74.7 428 15 US-10-369-493-16644 Sequence 55 66.3 366 12 US-10-369-493-30867 Sequence 55 66.3 449 15 US-10-369-493-308 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence 53 63.3 599 15 US-10-369-493-17361 Sequence 53 63.4 678 15 US-10-369-493-19361 Sequence 53 63.4 678 15 US-10-369	80 96.4 55.5 14 US-10-218-743-18 Sequence 62 74.7 428 15 US-10-369-493-1664 Sequence 55 66.3 366 12 US-10-424-599-209667 Sequence 55 66.3 449 15 US-10-369-493-3008 Sequence 55 66.3 572 15 US-10-369-493-1858 Sequence 56.3 599 15 US-10-369-493-17162 Sequence 57 67 78 78 78 78 78 78 78 78 78 78 78 78 78	80 96.4 555 14 US-10-218-743-15 Sequence 90.96.4 555 14 US-10-218-743-18 Sequence 62 74.7 428 15 US-10-369-493-16644 Sequence 55 66.3 366 12 US-10-424-599-209667 Sequence 55 66.3 572 15 US-10-369-493-18585 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 53 63.9 357 15 US-10-369-493-17162 Sequence 53 63.9 357 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-49	80 96.4 536 14 US-10-218-743-21 80 96.4 555 14 US-10-218-743-18 80 96.4 555 15 US-10-369-493-16644 Sequence 62 74.7 428 15 US-10-369-493-30867 Sequence 55 66.3 366 12 US-10-369-493-308 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence	80 96.4 509 14 US-10-218-743-38 Sequence 80 96.4 536 14 US-10-218-743-15 Sequence 80 96.4 555 14 US-10-218-743-15 Sequence 80 96.4 555 14 US-10-218-743-18 Sequence 80 96.4 555 14 US-10-218-743-18 Sequence 62 74.7 428 15 US-10-369-493-16644 Sequence 55 66.3 366 12 US-10-424-599-209667 Sequence 55 66.3 449 15 US-10-369-493-3088 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence	80 96.4 509 14 US-10-218-743-35 Sequence 80 96.4 509 14 US-10-218-743-31 Sequence 80 96.4 536 14 US-10-218-743-21 Sequence 80 96.4 536 14 US-10-218-743-15 Sequence 80 96.4 555 14 US-10-218-743-15 Sequence 80 96.4 555 14 US-10-218-743-15 Sequence 62 74.7 428 15 US-10-369-493-18644 Sequence 55 66.3 366 12 US-10-424-599-209667 Sequence 55 66.3 572 15 US-10-369-493-18585 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 57 673-783-783-783-783-783-783-783-783-783-7	80 96.4 490 14 US-10-218-743-41 Sequence 80 96.4 509 14 US-10-218-743-35 Sequence 80 96.4 509 14 US-10-218-743-38 Sequence 80 96.4 509 14 US-10-218-743-38 Sequence 80 96.4 536 14 US-10-218-743-21 Sequence 80 96.4 555 14 US-10-218-743-18 Sequence 62 74.7 428 15 US-10-369-493-1664 Sequence 55 66.3 366 12 US-10-369-493-1864 Sequence 55 66.3 572 15 US-10-369-493-1858 Sequence 55 66.3 572 15 US-10-369-493-1858 Sequence 55 66.3 572 15 US-10-369-493-1858 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 57 673 673 674 678 18 US-10-369-493-17162 Sequence 58 673 673 18 US-10-369-493-17162 Sequence 59 673 673 673 673 673 673 673 673 673 673	81 97.6 17 14 US-10-218-743-10 Sequence 80 96.4 490 14 US-10-218-743-41 Sequence 80 96.4 509 14 US-10-218-743-35 Sequence 80 96.4 509 14 US-10-218-743-38 Sequence 80 96.4 509 14 US-10-218-743-18 Sequence 80 96.4 536 14 US-10-218-743-11 Sequence 80 96.4 555 14 US-10-218-743-18 Sequence 62 74.7 428 15 US-10-218-743-18 Sequence 62 74.7 428 15 US-10-369-493-1664 Sequence 55 66.3 366 12 US-10-369-493-1858 Sequence 55 66.3 572 15 US-10-369-493-1858 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 55 66.3 572 15 US-10-369-493-17162 Sequence 55 66.3 599 15 US-10-369-493-17162 Sequence 55 66.3 592 15 US-10-369-493-17162 Sequence 55 66.3 592 15 US-10-369-493-17162 Sequence

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# ALIGNMENTS

RESULT 1

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FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT APPLICATION NUMBER: US/99/292,225
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR PILING DATE: 1998-09-02
PRIOR PILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-04-17
PRIOR PILING DATE: 1998-04-17
PRIOR PILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR PILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR PILING DATE: 1998-04-17
VUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTING DATE: 1998-04-17
TYPE: PRT
ORGANISM: Dermatophagoides farinae
PEATURE:
OTHER INFORMATION: At location 14, Xaa
US-10-218-743-10
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Publication No. US20030096779A1
GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 17; Conserval
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
          97.6%; Score 81; DB 14; ilarity 100.0%; Pred. No. 8.7e-08; Conservative 0; Mismatches 0;
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-41
                                                                                                                                           PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
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Best Local :
                                                                         SOFTWARE: P
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Publication No.
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PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
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PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
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CURRENT FILING DATE: 2002-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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CURRENT FILING DATE: 2002-08-13
                                                                                                                             NUMBER OF SEQ ID NOS: 49
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PRIOR FILING DATE: 1998-04-17
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PRIOR FILING DATE: 1999-04-15
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TYPE: PRT
ORGANISM: Dermatophagoides farinae
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                                                                                                  PatentIn Ver. 2.0
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94.1%;
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Pred. No. 5.2e-06;
0; Mismatches 1
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US-10-218-743-38
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10218743

Publication No. US20030096779A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
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SEQ ID NO 38
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Best Local Similarity
Matches 16; Conserv
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CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
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PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
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CURRENT FILING DATE: 2002-08-13
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APPLICANT: Weber, Eric R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATION NUMBER: 09/062,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10218743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10218743
to. US20030096779A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shirley Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.48;
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; Pred. No. 5.4e
0; Mismatches
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Pred. No. 5.4e-06;
0; Mismatches
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APPLICATION NUMBER:

60/098,565

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RESULT 7
US-10-218-743-18
(S-10-218-743-18
; Sequence 18, Application US/10218743
; Publication No. US20030096779A1
; Publication No. US20030096779A1
; GENERAL INFORMATION:
    MCCall, Catherine A.
    APPLICANT: McCall, Catherine A.
    APPLICANT: Hunter, Shirley Mu
; APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: ADD USES THEREOF
FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
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SEQ ID NO 15
LENGTH: 555
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NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Publication No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/08,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3 CURRENT APPLICATION NUMBER: US/10/218,743 CURRENT FILING DATE: 2002-08-13 CURRENT FILING DATE: 2002-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McCall APPLICANT: Hunte: APPLICANT: Weber
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PRIOR FILING DATE: 1998-04-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/098,565
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                                                                                                                                                                                                                                                                                                                                                              273
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                                                                                                                                                                                                                                                                                                                                                            DKLVMGVPFYGRAWSIE 289
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Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10218743
No. US20030096779A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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r, Shirley Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.4%; Score 80; DB 14; 94.1%; Pred. No. 5.9e-06;
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94.18;
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Pred. No.
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5.7e-06;
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PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILLING DATE: 1998-09-02
PRIOR FILLING DATE: 1998-05-13
PRIOR FILLING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILLING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILLING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 555
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US-10-424-599-209667
, Sequence 209667, Application US/10424599
, Publication No. US20040031072A1
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LENGTH: 428
                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local (
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Best Local
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                              178 DKLVLGVPFYGR 189
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                                                                                                                                                                                                                                                                                                                                                                                                        1 DKLVMGVPFYGR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.7%;
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Pred. No. 0.0083;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3308
LENGTH: 449
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US-10-424-599-209667
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          TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052)8

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR ETLING DATE: 2002-02-21

NUMBER OF SEG ID NOS: 47374
EQ ID NO 18585
                                                                                                                                                                               APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                10-369-493-18585
                                                                                                                                                                                                                                                                                                          equence 18585, Application US/10369493 ublication No. US20030233675A1
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LOCATION: (1)..(449)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Neurospora crassa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
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les 9; Conserv
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66.7%;
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Pred. No. 0.13
3; Mismatches
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Pred. No.
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Bacillus halodurans US-10-369-493-17162
                                                                US-10-369-493-19361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-369-493-19361
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                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19361
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17162, Application US/10369493 Publication No. US20030233675A1
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Best Local
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Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
RICH RAPPLICATION NUMBER: US 60/360,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                             LENGTH: 392
TYPE: PRT
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPPLICANT: Cao, Yongwei
RPPLICANT: Hinkle, Gregory J
RPPLICANT: Slater, Steven C.
RPPLICANT: Goldman, Barry S.
RPPLICANT: Chen, Xianfeng
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TYPE: PRT
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10; Conservative
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71.4%;
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Pred. No. 0.
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Pred. No. 0
    Score 53; DB 15; Pred. No. 0.33;
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                   Length 392;
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APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Composit.
TITLE OF INVENTION: Methods of Screening for Modulators of FILD REFERENCE: 018501-012500US
CURRENT APPLICATION UNMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/350,366
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
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LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-632
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US-09-459-749D-17
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US-10-295-027-632
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GENERAL INFORMATION:
APPLICANT: Millis, Albert J. T.
TITLE OF INVENTION: Compositions and Methods For Altering Cell Migration
FILE REFERENCE: 0794.016A
                                                                                                     Sequence 17, Application US/09459749D Patent No. US20020136716A1
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Best Local (
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: US 60/332,464
OR FILING DATE: 2001-11-21
OR APPLICATION NUMBER: US 60/334,393
OR FILING DATE: 2001-11-29
OR APPLICATION NUMBER: US 60/340,376
OR FILING DATE: 2001-12-14
OR APPLICATION NUMBER: US 60/347,211
OR FILING DATE: 2002-01-08
OR APPLICATION NUMBER: US 60/347,349
OR APPLICATION NUMBER: US 60/347,349
OR FILING DATE: 2002-01-10
OR FILING DATE: 2002-01-10
OR FILING DATE: 2002-01-02
OR FILING DATE: 2002-01-03
OR PILING DATE: 2002-01-03
OR PILING DATE: 2002-01-03
OR APPLICATION NUMBER: US 60/355,250
OR APPLICATION NUMBER: US 60/356,714
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254 EKLIMGIPTYGR 265
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Similarity 66.7%;
8; Conservative
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Hevezi, Peter A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aziz, Natasha
Ginsberg, Wendy M.
Gish, Kurt C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murray, Richard
Watson, Susan R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mack, David H.
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CURRENT APPLICATION NUMBER: US/09/459,749D

CURRENT FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 60/111,856

PRIOR FILING DATE: 1998-12-11

NUMBER OF SEQ ID NOS: 17

SOOTWARE: Patentin Ver. 2.1

SEQ ID NO 17

LENGTH: 383

TYPE: PRT

CORGANISM: Sus scrofa

US-09-459-749D-17

Query Match
Best Local Similarity 50.0%; Pred. No. 1.1;

Matches 8; Conservative 6; Mismatches 2; Indels 0;

Matches 8; Conservative 6; Mismatches 2; Indels 0;

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1 DKLVMGVPFYGRAXSI 16

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Gaps

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Search completed: March 22, 2004, 07:45:49
Job time: 3.47749 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Listing first 45 summaries
                                                                                                                                            Issued_Patents_AA:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

27	26	25	24	23	22	21	. 20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	ហ	4.	ω	N	ч	Result No.
47	47	47	47	48	49	49	49	49	49	50	52	52	56	58	58	59	59	59	59	80	80	80	80	80	80	81	Score
	σ,	9	6	7.	9	9	9	9	9			62.7	7.	9	۴	۲			71.1	σ,	<u>ب</u>	σ.	96.4			7.	Query Match
373	373	373	16	170	424	424	424	399	399	383	377	371	635	554	554	583	583	559	489	555	555	536	509	509	490	17	Length I
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-08-877-599-1	US-09-039-198A-15	39-198A-	05 - 3	09-2	T-US94-01198-	-371-680-	-08-0	-649-747A-	-09-649-747	-09-459-749D-	8-591-629-	1-62	45-814-	-09-052-778-1	-08-524-051-	9-545-814-	45-814-	9-545-814-	-09-545-814-2	9-292-225-	-09-292-225-1	-09-292-225-2	9-292-225-3	25-3	-09-292-225-4	9-292-225-	ID
equence 1	e 15	e 14	e 39	equence 44	e 2, Appl	e 2, Appl	equence 2,	e 19, App	Ľ	17	e 8, Appl	Sequence 2, Appli	32, App	16	2	•	2	equence 14, App	e 29, App	equence 18	equence 15	equence 21	e 38	equence 35, App	equence 41	uence 10	Description

Sequence 41, Application US/0929225
Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	α.
47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	4/
56.6	-	56.6		-	•	•		•	•		•		56.6	•	•		٠
466	466	466	466	466	423	423	423	416	389	389	387	387	387	385	373	373	3/3
4.	ω	w	w	N	4,	مر	μ	N	w	μ.	4	w	N	N	4	4	4
US-09-343-623-4	US-09-039-198A-4	US-09-039-198A-2	US-09-151-011-4	US-08-486-839-4	US-08-850-348A-2	US-07-939-501A-12	US-07-939-501A-10	US-08-694-915-4	US-08-448-398-7	US-07-939-501A-1	US-09-343-623-6	US-09-151-011-6	US-08-486-839-6	US-08-694-915-2	267-574-	US-09-267-574-14	GT-669-7.7.8-80-SD
Sequence 4, App	Sequence 4, App	Sequence 2, Appli	Sequence 4, App.	Seguence 4, App	Sequence 2, Appli	Sequence 12, App.	Sequence 10, Ap	Sequence 4, App	Sequence 7, App	Sequence 1, Appl:	Sequence 6, Appli	Sequence 6, Appl	Sequence 6, Appl	Sequence 2, App	ш	Sequence 14, Ap	sequence 15, App

# ALIGNMENTS

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US-09-292-225-10
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RESULT 2
US-09-292-225-41
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Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 10
LENGTH: 17
                                                                                                                                                                                          Matches
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Dermatophagoides farinae
FEATURE:
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Conservative
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; Pred. No.
                                                                                                                                                                                          Mismatches
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1e-08;
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; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-41
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US-09-292-225-38
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EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-3
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION DATE: 1998-04-17
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
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Best Local Similarity
Matches 16; Conser
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SEQ ID NO 35
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Best Local Similarity
                                                                 Sequence 38, Application US/09292225 Patent No. 6455686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
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CURRENT APPLICATION NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ
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                                                                                                                                                                                        273
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o. 6455686
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94.1%;
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Pred. No.
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Pred. No. 7.
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8.1e-07;
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; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38
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SEQ ID NO 38
SEQ TH: 509
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 536
TYPE: PRT
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Patent No. 645568
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                                                                                                                        Query Match
                                                                                                                                                                 ORGANISM: Dermatophagoides farinae -09-292-225-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McCall, Catherine A.
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NUMBER OF SEQ ID NOS: 49
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254 DKĽVMGVPFYGRAWSIE
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                                        1 DKLVMGVPFYGRAXSIE 17
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                                                                               Similarity 94...
16; Conservative
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                                                                                                  96.4%;
94.1%;
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270
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Pred. No.
                                                                                                  Score 80;
Pred. No.
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RESULT 6 US-09-292-225-15

Sequence 15, Application US/09292225 Patent No. 6455686

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; TYPE: PRT ; ORGANISM: Dermatophagoides farinae US-09-292-225-18
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CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
                                                                                                                Query Match
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SEQ ID NO 18
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Best Local Similarity
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                                                                              Matches
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Heber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
CURRENT APPLICATION NUMBER: 60/098,909
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EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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APPLICANT: Hunter, Shirley Mu
APPLICANT: Hunter, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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EARLIER APPLICATION NUMBER: 60/085,295
EARLIER RETLING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
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16; Conserv
  DKL/VMGVPFYGRAWSIE 289
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                                    DKLVMGVPFYGRAXSIE 17
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94.1%;
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Pred. No.
                                                                                                Score 80;
Pred. No.
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                                                                              Mismatches
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. 9e-07;
                                                                                                DB 4;
9e-07;
                                                                                                                Length 555;
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RESULT 8

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; ORGANISM: Tagged Ctenocephalides felis
US-09-545-814-29
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US-09-545-814-14
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US-09-545-814-2
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                                                                                                   GENERAL INFORMATION:
APPLICANT: Becher, A
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 559
TYPE: PRT
ORGANISM: Ctenocephalides felis
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Best Local Similarity
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SEQ ID NO 29
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Patent No. 6416977
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: FLEA CHITINASE NUCLE:
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,833
PRIOR FILING DATE: 1999-04-09
FILE REFERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,833
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILING DATE: 2000-04-07
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                                                                                                           USES THEREOF
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                                                                                                                             FLEA CHITINASE NUCLEIC
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62.5%;
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62.5%; Pred. No. 0.
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Pred. No.
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                                                                                                                             ACID MOLECULES, PROTEINS
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US-08-524-051-2
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US-09-545-814-5
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TYPE: PRT
; ORGANIEM: Ctenocephalides felis
US-09-545-814-2
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SEQ ID NO 5
LENGTH: 583
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GENERAL INFORMATION:
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APPLICANT: Becher,
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Best Local Similarity 62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,833
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 40
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TITLE OF INVENTION: FLEA CHITINA
TITLE OF INVENTION: USES THEREOF
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IF Compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         APPLICANT: Corpuz, Lolita
APPLICANT: Gopalakrishnan, Bhuvana
TITLE OF INVENTION: RECOMBINANT CHITINASE AND USE THEREOF AS
TITLE OF INVENTION: A BIOCIDE
                                                                                                                                                                                                     ADDRESSEE: Hovey, Wi
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                         STREET:
 APPLICATION NUMBER:
                                                                                                                                       COUNTRY:
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                                                                                                                     64108
                                                                                                                                                                SSEE: Hovey, Williams, Timmons & Collins
T: 2405 Grand Blvd., Suite 400
Kansas City
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                                                                                                                                       USA
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Muthukrishnan, Subbaratnam
Choi, Hee Kyung
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US/08/524,051
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GENERAL INFORMATION:
APPLICANT: Bryant, Peter J.
APPLICANT: Kawamura, Kazuo
ITILE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS
ITILE OF INVENTION: OF USE
FILE REFERENCE: 07306/015001
CURRENT APPLICATION NUMBER: US/09/052,778A
CURRENT FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 554
                                     GENERAL INFORMATION:
APPLICANT: Becher, Anna M.
TITLE OF INVENTION: FLEA CHITINASE NUCLEIC
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: FC-5-C1
CURRENT APPLICATION NUMBER: US/09/545,814
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,833
PRIOR FILING DATE: 1999-04-09
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Patent No. 60605
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Matches 9; Conserv
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NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin "--
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Manduca sexta
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TYPE: amino acid
TOPOLLOGY: linear
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REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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CLASSIFICATION:
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milarity 56.2%;
Conservative
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(816)474-9057
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56.2%;
                                                                                                                                          CHITINASE NUCLEIC
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Pred. No.
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Pred. No.
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0.012;
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                                                                                                                                        ACID MOLECULES,
                                                                                                                                                                                                                                                                                                                                                                                       Length 554;
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SEQ ID NO 32 LENGTH: 635

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; TYPE: PRT
; ORGANISM: Tagged Ctenocephalides felis
US-09-545-814-32
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US-08-591-629-2
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                                                                                                                                                               , MOLECULE TYPE: protein US-08-591-629-2
                                                                             Query Match 62.7%; Score 52; DB 2; Best Local Similarity 75.0%; Pred. No. 0.1; Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08591629
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Best Local Similarity 83.7
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                    APPLICATION UNMEER: US/08/591,629
FILING DATE: 15-FEB-96
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02761
FILING DATE: 17-AUG-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 93202425.0
FILING DATE: 17-AUG-93
ATTORNEY/AGENT INFORMATION:
NAME: MASS, CLIFFORD J.
REGISTRATION NUMBER: U-010627-0
REFERENCE/DOCKET NUMBER: U-010627-0
TELECOMMUNICATION INDEER: U-010627-0
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 708-1800
TELEPAN: (212) 246-8959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: MELCHERS, Leo Sjoerd

APPLICANT: MELCHERS, Leo Sjoerd

APPLICANT: MOINT APOTHEKER-DE GROOT, Marion

APPLICANT: LONG Ferdinand

APPLICANT: CORNELISSEN, Bernardus Johannes Clemens

APPLICANT: LINTHORST, Hubertus Josephus Maria

APPLICANT: PONSTEIN, Anne Silene

APPLICANT: SELA-BUURLAGE, Marianne Beatrix

TITLE OF INVENTION: Plants containing same

NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10033-7604
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: IBM PC 4.86 SX 50 Mhz
OPERATING SYSTEM: DOS 6.20
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          TELEX: 233288
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Ladas & Parry
STREET: 26 West 61st Street
CITY: New York
STRIE: NY
COUNTPY
                                                                                                                                                                                                                                                                                         TELEFAX: \__
TELEFAX: \__
233288
                                                                                                                                                                                                     LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
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2 KLVMGVPFYGRA 13
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245 KLVLGIPFYGYA 256
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Search completed: March 22, 2004, 07:03:57 Job time : 2.37021 secs

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Result
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Perfect score:
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109
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Maximum Match 100%
Listing first 45 summaries
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pir4:*
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   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
                   T44445
AE1494
S53990
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                                                                                                                                                     transcription regularity E1A 20K protlag-2 protein - Ca T1K7.9 protein - A hypothetical proteinsecticidal toxin probable ribosomal
xylan 1,4-beta-xyl hypothetical prote AcOrf-150 protein
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shikimate 5-dehydr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1635 <DEL>
A;Cross-references: EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AAB81850.1
C;Genetics:

A; Gene: CHT2

A; Reference number: Z17872 A; Accession: T14075

### ALIGNMENTS

RESULT 1
T14075
Chitinase (EC 3.2.1.14) - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999
C;Accession: T14075
C;Accession: T14075
R;de la Vega, H; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.

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exicionase - Lactobacillus phage phi-gle
C;Species: Lactobacillus phage phi-gle
C;Species: Lactobacillus phage phi-gle
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C;Accession: T13181
R;Kodaira, K.I.; Oki, M.; Kakikawa, M.; Watanabe, N.; Hirakawa, M.; Yamada, K.; Taketo,
Gene 187, 45-53, 1997
A;Title: Genome structure of the Lactobacillus temperate phage phi gle: the whole genom
A;Reference number: Z17831; MUID:97225795; PMID:9073065
A;Accession: T13181
                                                                                         A; Molecule type: DA
A; Residues: 1-66 < KOD>
A; Cross-references: EMBL: X98106;
C; Genetics:
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                                                                          A;Gene: Xis
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                      Query Match
Best Local :
     Matches
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     Similarity 9; Conserv
     Conservative
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                     49.1%;
50.0%;
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                                                                                                         NID:e917136; PID:e247183; PIDN:CAA66757.1
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Pred. No. 2;
                     Score 53.5; DB Pred. No. 0.19;
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     Mismatches
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1 DIPHPTNI---HKYLVCE

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ok, C.; Schlueter, T.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; A, Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1136
A,Scatuer number: AC1136
                                                                                                                   RESULT 5
AE1494
                                                                                                                                                                                                                                                                                                                                                                                                    A; Nolecule type: DNA
A; Residues: 1-291 <GLA>
A; Residues: 1-291 <GLA>
A; Cross-references: GB:NC_003210;
A; Cross-references: Strain EGD-
                 shikimate 5-dehydrogenase homolog lin0493 [imported] - Listeria innocua (st C;Species: Listeria innocua (st C;Species: Listeria innocua (c;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 07-Jul-2003 C;Accession: AE1494 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche,
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C;Keywords: glycosidase; hydrolase
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A;Residues: 1-525 <SHE>
A;Cross-references: EMBL:AF008575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Shen, Z; Jacobs-Lorena, M.
R;Shen, Z; Jacobs-Lorena, M.
submitted to the EMBL Data Library, June 1997
A:Reference number: Z22771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chitinase (EC 3.2.1.14) [imported] - African malaria mosquito
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text_change 21-Jan-2000
C;Date: 7. TAAAAA
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A;Accession: T44445
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Best Local (
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   Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
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Bernal, G.; Duc
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72.7%;
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53.8%;
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Pred. No. 1.9;
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                                                                                              [imported] - Listeria innocua (strain
                                                                                                                                                                                                                                                                                  DB
9.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , A.; Baquero, I
Dussurget, O.;
                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g16409866;
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                                                                                                                                                                                                                                                                                                                                               dehydrogenase
                                                                                                                                                                                                                                                                                                        Length 291;
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F.; Berche, P.; ; Entian, K.D.; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F.; Berche, P.; ; Entian, K.D.;
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 ; Bloecker
Fsihi, H.
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Fsihi, H.
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 glycoprotein H - human herpesvirus 3
N,Alternate names: glycoprotein III
C;Species: human herpesvirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #tex
C;Accession: B27341
R;Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
                                                                                                                                       RESULT 7
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A;Cross-references: EMBL:X82444; NID:g563910; PIDN:CAA57824.1; PI R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; submitted to the EMBL Data Library, July 1999
A;Reference number: Z21880
A;Accession: T39793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA methyltransferase pmt1 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-2000
C;Accession: S53990; T39793
R;Wilkinson, C.R.M.; Bartlett, R.; Nurse, P.; Bird, A.P.
Nucleic Acids Res. 23, 203-210, 1995
A;Title: The fission yeast gene pmt1(+) encodes a DNA methyltransferase home
A;Reference number: S53990; MUID:95166638; PMID:7862522
A;Accession: S53990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL592022; pIDN:CAC95725.1; pID:g16412933; A;Experimental source: strain Clip11262 C;Genetics: A;Gene: lin0493 C;Superfamily: shikimate 5-dehydrogenase; shikimate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1494
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-291 <GLA>
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A; Residues: 1-330 <WIL>
                                                                                                                                                                     A; Introns:
C; Superfam:
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A; Introns: 56/3
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A;Experimental source: strain 972h-; cosmid c19C2
                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-330 < MCD>
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Best Local S
Matches 7
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Best Local S
Matches 8
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les 8; Conserv
108 LPHVNNLPEYILIENVOG 125
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7; Conserve
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                                       IPHPTNIHKYLVCESVNG 19
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Pred. No.
                                                                                                       Score 47;
Pred. No.
                                                                                   Mismatches
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9.1;
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Voss, H.; Wehland,
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30-Sep-1988 #text\_change 16-Jul-1999

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A;Gene:
C;Superf
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J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori r
A:Reference number: Z22020; MUID:99281911; PMID:10355780
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C;Species: Rickettsia prowazekii
C;Datc: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
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                                                                                                      A;Cross-references: EMBL:L33180; PIDN:AAC63816.1
A;Experimental source: isolate T3
                                                                                                                                                      A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                                                                                         A; Reference number: Z22020;
A; Accession: T41887
                                                                                                                                                                                                                                                                            A;Variety: isolate T3
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: T41887
                                                                                                                                                                                                                                                                                                                            AcMNPV orf150 - Bombyx mori nuclear polyhedrosis virus (isolate C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; A;Experimental source: strain Madrid E
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R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.;
Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-841 <DAV>
A;Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27920.1;
C;Genetics:
                                                                 A; Note: Orf_126
                                                                                                                                        A;Residues: 1-115 <KAM>
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A;Reference number: A71630; MUID:99039499; PMID:9823893
                                                                                                  A; Experimental source:
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Score 45; DB Pred. No. 7.2; 4; Mismatches
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, March
A;Reference number: Z21904
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A;Molecule type: DNA
A;Residues: 1-342 <LYN>
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                                                                                                  Similarity 6; Conserv
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                               PHPTDCHLFIQC 470
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C;Species: Brugia malayi
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A38221
R;Fuhrman, J.A.; Lane, W.S.; Smith, R.F.; Piessens, W.F.; Perler, F.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 1548-1552, 1992
A;Title: Transmission-blocking antibodies recognize microfilarial chitinase in brugian 1 A;Reference number: A38221; MUID:92179220; PMID:1542646
A;Accession: A38221
A;Accession: A38221
                                                                                                                               A;Cross-references: GB:M73689; NID:g156063; PIDN:AAA27854.1; PID:g156064
A;Note: sequence extracted from NCBI backbone (NCBIP:85345)
C;Keywords: g1ycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                       A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid; protein A;Residues: 1-504 <FUH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chitinase (EC 3.2.1.14) MF1 - nematode (Brugia malayı)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fission yeast (Schizosaccharomyces pombe)
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rch 1998
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-523 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable ubiquitin activating enzyme [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A84420;
A; Accession: G84732
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A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                              transcription regulator (phage-related) (Xre family) [imported] - Clostridium acetobuty: C_iSpecies: Clostridium acetobutylicum
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                                      R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
                                                                                      C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D97130
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;Residues: 1-867 <SMW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iant Mól. Biól. 28, 443-454, 1995
;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein;Reference number: S57795; MUID:95359403; PMID:7632915;Accession: S57795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-867 <SMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Molecule type: DNA
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Accession: S66368
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Best Local
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Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
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                        nett, G.N.; Koonin,
4823-4838, 2001
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Ba0010
Barly ElA 20K protein - canine adenovirus 2
C;Species: Mastadenovirus can2 (canine adenovirus 2)
A;Note: host Canis lupis familiaris (dog)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #
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A;Cross-references: GB:AE001437; PIDN:AAK79831.1; PID:g15024845; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
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A;Accession: D97130
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
                                                   Query Match
Best Local Similarity
Thes 9; Conserve
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Virus Res. 14, 241-256, 1989
A;Title: Identification and nucleotide sequence of the early region 1 from canine adenov.
A;Reference number: A60010; MUID:90163565; PMID:2623943
A;Accession: B60010
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                                                                                                                                       C;Superfamily: adenovirus early ElA protein C;Keywords: early protein; transcription regulation
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A; Residues: 1-171 <SPI>
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P4099 schizosacch
P09260 varicella-z
O76217 anopheles g
Q9zdf1 rickettsia
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drosophila
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40.5	41	41	41	41	41	41	41	41	41	41	41
37.2	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6
232	926	576	290	290	260	258	257	252	251	251	202
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VSPA_BOTJA	RPM1 ARATH	CBPS_YEAST	KDSA_PEA	KDSA_ARATH	VSP6_TRIMU	VSP3_BOTJA	VSP2_BOTJA	TPIS STRPN	TPIS_STRPY	TPIS_STRP8	ADEN_ADEB7
	Q39214 arabidopsis	P27614 saccharomyc	O50044 pisum sativ	Q9av97 a 2-dehydro	Q9dg83 trimeresuru	Q9ptu8 bothrops ja	_		P82478 streptococc	Q8p1w3 streptococc	P19151 bovine aden

### ALIGNMENTS

RESULTIN RAGE_LISIN STANDARD; PRT; 291 AA. RAGE_LISIN STANDARD; PRT; 291 AA. RAGE_LISIN STANDARD; PRT; 291 AA. RAGE_COR_LISIN STANDARD; PRT; 291 AA. RAGE_COR_LING493.  S1.Listeria innocua. CS ARCE_COR_LING493. CS Listeria innocua. CS ARCE_COR_LING493. CS LISTER_COGO (Rel. 41, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last sequence update) RR ARCE_LISTER_CORNEAL (Rel. 41, Last sequence update) RR Remmell B., Rose M., Schlueter T., Simoes M., Tierrez A., RR ARCE_CORNEAL (Rel. 41, Last sequence update) RR ARCE_CORNEAL (Rel. 41, Last sequence update) RR Remmell B., Rose M., Schlueter T., Simoes M., Tierrez A., RR ARCE_CORNEAL (Rel. 41, Last sequence update) RR Remmell B., Rose M., Schlueter T., Simoes M., Tierrez A., RR ARCE_CORNEAL (Rel. 41, Last sequence update) RR Remmell B., Rose M., Schlueter T., Simoes M., Tierrez A., RR ARCE_CORNEAL (Rel. 41, Last sequence update) RR Remmell B., Rose M., Schlueter T., Simoes M., Tierrez A., RR Maduenc E., Danid Schluete Schluete + MADP(+) = 5-dehydroshikimate + C., RR ARCE_CORNEAL (Rel. 41, Last sequence update) RR Rel. Rel. Rel. Rel. Rel. Rel. Rel. Re
ISIN ROE_LISIN STANDARD; PRT; 291 AA. 2267; 2267; 25783-2003 (Rel. 41, Last sequence update) 6-788-2003 (Rel. 41, Last sequence update) 6-788-2013 (Rel. 41, Last sequence update) 7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-

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Best Local
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
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Shikimate 5-dehydrogenase (EC 1.1.1.25)
AROS OR LM00490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294:849-852(2001).
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Bacteria; Firmicutes; I
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SEQUENCE 291 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00222; -; 1.
InterPro; IPR006151; Shikimate_DH.
Pfam; PF01488; Shikimate_DH; 1.
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"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
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      (Rel. 31, Created)
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79; PubMed=11679669;
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RA Wood V. Gwilliam R. Rajandream M.A. Lyne M., Lyne M., Stewart A., RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gonlies M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA James K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., RA Mooney P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C., RA RA Noncey P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C., RA RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sharp S., RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller H., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Rh Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Rh Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Rh Shakovski G.V., Ussery D., Barrell B.G., Nurse P.; RT "The genome sequence of Schizosaccharomyces pombe.";
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STRAIN=97
                                                                                                                                                                                                                                                                                                     MEDIINE=96194447; PubMed=8636983;
Pinarbasi E., Ellictt J., Hornby D.P.;
"Activation of a yeast pseudo DNA methyltransferase by deletio
single amino acid.";
J. Mol. Biol. 257:804-813(1996).
-!- FUNCTION: Does not have a cytosine-5 methyltransferase act
due to the insertion of a Ser residue between the Pro-Cys
found at the active site of C5 MTases. When this serine is
it becomes catalytically active and recognizes and methyla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA methyltransferase PMT1 OR SPBC19C2.02.
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilkinson C.R.M., I "The fission yeast homologue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE=21848401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 23:203-210(1995).
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                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Belongs to the C5-methyltransferase family.
                                                                                                                                                                                                                                                                                        sequence CC[AT]GG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=7862522;
Bartlett R., Nu
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homolog pmtl (SpIM.Spol)
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NA methyltransferase
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EMBL; X82444; CAA57824.1; -. EMBL; AL109731; CAB52029.1;

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GeneDB SPombe; SPBC19C2.02; ...
InterPro; IPR001525; C5_DNA_meth.
Pfam; PF00145; DNA_methylase; 1.
PRINTS; PR00105; C5_MTTRPAASE.
PROSITE; PS00094; C5_MTASE_1; FALSE_NEG.
PROSITE; PS00095; C5_MTASE_2; 1.
                                                                                         SEQUENCE
                                                                                                                                                                                                     Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        EMBL; X04370;
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01-MAR-1989 (Rel. 10, Last sequence update)
16-CCT-2001 (Rel. 40, Last amoutation update)
Probable glycoprotein H precursor (Glycoprotein
                                                                                                                                                                                                                               PIR; B27341; VGBE37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Varicella-zoster virus (strain Dumas) (VZV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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REBASE; 2888; M.SpomI
                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the herpesviruses glycoprotein H family.
                                                                                                                                                                                                                                                                                                                                                                                         Davison A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE=86306657; PubMed=3018124;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGLH_VZVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                    son A.J., Scott J.E.;
complete DNA sequence of varicella-zoster virus.";
en: Virol. 67:1759-1816(1986).
715
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                      IPHPTNIHKYLVCESV 17
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5; Mismatches
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SMART; SM00494; ChtBD2; 2.

PROSITE; P850940; CHIT_BIND_II; 2

Chitin-binding; Glycoprotein; Rep
SIGNAL 1 17

CHAIN 18 153

DOMAIN 18 79

CARBOHYD 63 63 N-LII

CARBOHYD 63 63 N-LII
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DOMAIN
CARBOHYD
SEQUENCE
                        Rickettsia prowazekii.
Bacteria; Proteobacteria;
Rickettsiaceae; Rickettsi
                                                                                                                                                         16-OCT 2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
CTP synthase (EC 6.3.4.2) (UTP--ammoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A type I peritrophic matrix protein from the malaria vector Anophelo gambiae binds to chitin. Cloning, expression, and characterization.", S. Biol. Chem. 273:17665-17670(1998).
-i- FUNCTION: Binds chitin but not cellulose. May be involved in the spatial organization of pm.
-i- TISSUB SPECIFICITY: Adult peritrophic membrane.
-i- DEVELOPMENTAL STACE: Expressed in adult but not larval guts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shen
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InterPro; IPR002557; Chitin_bind_PerA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inso
Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Contains 2 chitin-binding type-2 domains.
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MEDLINE=98316335; PubMed=9651363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                           Alphaproteobacteria; eae; Rickettsia.
                                                                                                                                                  c annotation update)
(UTP--ammonia ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PERITROPHIN-1.

PERITROPHIN-1.

CHITIN-BINDING TYPE-2 1.

CHITIN-BINDING TYPE-2 2.

N-LINKED (GLCNAC. . .) (POT N. . . .) (POT N. . . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; I
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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era; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  malaria vector Anopheles
and characterization.";
                                                              Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 153
                                                                                                                                                                    (CTP synthetase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Rickettsieae;

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RESULT
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Best Local S
Matches
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Pfam; PF00117; GATAse; 1.

TIGREAMS; TIGR00337; PyrG; 1.

TIGREAMS; TIGR01045; RPB; 1.

TIGREAMS; TIGR01045; GATASE TYPE I; 1.

PROSITE; PS00442; GATASE Type I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin
mitochondria.";
YBSI SCHPO STANDARD; PRT; 342 AA O59681; Q9USX5; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                          DOMAIN
ACT_SITE
ACT_SITE
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Selfish DNA in protein-coding genes of Rickettsia.";
Science 290:347-350(2000).
-!- FUNCTION: Catalyzes the ATP-dependent amination of UTP to either L-glutamine or ammonia as the source of nitrogen (E
                                                                                                                                                                                                                                                                                                                                 Complete
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20485642; PubMed=11030655;
Ogata H., Audic S., Barbe V., Artiguenave F.,
Raoult D., Claverie J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP, MF 01227; atypical; 1.
InterPro; IPR000991; GATase_1.
InterPro; IPR004468; PyrG synth.
InterPro; IPR005728; Rickett_RPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ235271; CAA14837.1; -. PIR; C71695; C71695.
                                                                SCHPO
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).

CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate +
ENZYME REGULATION: Allosterically activated by GTP, when g
is the substrate. Inhibited by CTP (By similarity).

The substrate inhibited by CTP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Homotetramer (By similarity).
SIMILARITY: Belongs to the CTP synthase family.
SIMILARITY: Contains 1 type-1 glutamine amidotransferase
SIMILARITY: Contains 1 RPE1 insert domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (last) step.
                                                                                                                          115
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                                                                                                                                                     N
                                                                                                                                                                                 Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                  proteome.
                                                                                                                        IPHVTNIIKDFIMSNTNG
                                                                                                                                                     IPHPINIHKYLVCESVNG
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                                                                                                                                                                                                                                                          299
586
473
379
555
557
                                                                                                                                                                                                                                             66173 MW;
                                                                                                                                                                                             42.2%;
50.0%;
                                                                                                                                                                                                                                                       AMINATOR DOMAIN.
GLUTAMINE MIDOTRANSFERASE.
RPB1 INSERT.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
                                                                                                                                                                                 2
                                                                                                                                                                                 Score 46; DB Pred. No. 9; 2; Mismatches
                                                                                                                                                                                                                                             FA14C0879F457A0A

    Glutamine amidotransferase;

                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fournier
                                                                                                                                                                                  7.
                                                                                                                                                                                                             Length 586;
                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γB
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RESULT
CHI3_DR
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DT 10
DT 15
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                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last annotation update Hypothetical protein C18E5.01 in chromosome SPBC18E5.01 OR SPBC29A3.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                         Hypothetical DOMAIN :
                                                                                                                                                                                         EMBL; AL022299; CAA18396.1; EMBL; AL035077; CAA22661.1;
                                                                                                                                                SEQUENCE
                                         DROME
                                                                                 130
                                                                                                                                                                          SPombe; SPBC18E5.01;
                                                                                                                Similarity 7; Conserv
                                                                                                PHPTNIHKYLVC 14
                                                                                                                                                 342 AA;
                                                                                                                                                         163
                                                                                                                 Conservative
                                                                                                                                                                 protein
                                                                                                                                                                                  T40090
                                        STANDARD;
                                                                                                                                                168 P
38220 MW;
                                                                                                                        41.3%;
58.3%;
                                                                                                                 Score 45; DB 1
Pred. No. 7.3;
1; Mismatches
                                                                                                                                                 POLY-VAL.
AE39A39B053F704F CRC64;
                                         458
                                         ጅ
                                                                                                                                 1; Length 342;
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                                                                                                                 Gaps
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Q9W5U2; C17422; 10-CCT-2003 (Rel. 42, Created) 10-CCT-2003 (Rel. 42, Last sequence up 15-MAR-2004 (Rel. 43, Last annotation Probable chitinase 3 (EC 3.2.1.14).

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RESULT
CHIT_BR
ID CH
AC P2
DT 01
DT 01
                                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                         CHIT BRUMA
P29030;
01-DEC-1992
01-DEC-1992
                                                                                                                                                                               DOMAIN
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutes There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Berkeley;
MEDLINE-22426071; PubMed=12537574;
HOSKINE-22426071; PubMed=12537574;
HOSKINE-R., Smith C.D., Carlson J.W., Carvalho A.B., Halpern
Hoskins R.A., Smith C.D., Carlson J.W., Sullivan B.A., Sutton
Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                           Multigene
                                                                                                                                                                                                                                   PROSITE; PS50940; CHIT BIND II; 2.
PROSITE; PS01095; CHITINASE 18; FALSE NEG.
PYDROSITE; PS01095; CHITINASE 18; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila.";
Insect Mol. Biol. 7:233-239(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 182-294 FROM STRAIN=Canton-S;
                                                                                                                                                                                                                                                                       SMART; SM00494; ChtBD2;
SMART; SM00636; Glyco_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 2 chitin-binding type-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Chitinases are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98324849; PubMed=9662472;
de la Vega H., Specht C.A., Liu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assembly.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Heterochromatic sequences in a Drosophila whole-genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Karpen G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                           φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages acetyl-D-glucosamine polymers of chitin. SIMILARITY: Belongs to chitinase class II (family 18 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydrolases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
S
                                                                                           83
                                                                                                                                    l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG18140
                                                                                                             IPHPTNIHKYLVC
                                                                                                                                                                                                                          family; Repeat.
                                                                                                                                                                           74
295
458
 (Rel. 24, Created)
(Rel. 24, Last sequence update)
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3:RESEARCH0085.1-RESEARCH0085.16(2002)
                                                                                                                                                                                 A
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a multi-gene family
                                                                                                                                                                               58
128
295
52330
                                                                                                                                              41.3%;
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                                                                                                                                     <u>ب</u>
                                                                                                                                    Score 45; DB Pred. No. 10; 2; Mismatches
                                                                                                                                                                                          PROTON
                                                                                                                                                                                                     CHITIN-BINDING TYPE-2 1. CHITIN-BINDING TYPE-2 2.
                                                                                                                                                                                AA063190B7E96248 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in Aedes, Anopheles and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robbins P.W.;
                                  504
                                                                                                                                                           DB 1;
                                  8
                                                                                                                                                                                                                                       Chitin-binding;
                                                                                                                                                          Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains.
                                                                                                                                     Indels
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(Rel.

41, 41,

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Query Match
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00494; ChtBb2; 1. T
SMART; SM00636; Glyco 18; 1.
PROSITE; PS50940; CHIT BLND II; 1.
PROSITE; PS01099; CHITINASE 18; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-2004 (Rel. 43, Last annotation update) Endochitinase precursor (EC 3.2.1.14) (MF1 an Brugia malayi (Filarial nematode worm).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01607; CBM 14; 1.

Pfam; PF00704; Glyco hydro 18; 1.

ProDom; PD000471; Glyco hydro 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M73689; AAA27854.1; -. PIR; A38221; A38221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
entities requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL S
MEDLINE=92179220; PubMed=1542646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Onchocercidae; Brugia.
NCBI_TaxID=6279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mosquito vector during parasite development and transmission. CAPALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of Nacetyl-D-glucosamine polymers of chitin.

DEVELOPMENTAL STAGE: The appearance of the MF1 antigen corresponds the onset of the parasite's ability to infect the mosquit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: Known to bind calcium. SIMILARITY: Belongs to chitinase clas
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MISCELLANEOUS: Known
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                                                                                                                                                                                                                                                                              504 AA;
                                                                                                                                                                                            Conservative
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CATALYTIC.
SER/THR-RICH (LINKER).
SER/THR PROXIMATE T
3 X 14 AA APPROXIMATE T
CHITIN-BINDING TYPE-2.
PROTON DONOR (BY SIMILA
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                                                                                                                                                                                                              Score 45;
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  PRT;
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103
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chitinase
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Best Local S
Matches
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01-JUN-1994
01-JUN-1994
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P35981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 25586;
STRAIN-ATCC 25586;
MEDLINE-21886394; PubMed=11889109;
MEDLINE-1 'V Anderson I., Ivanova N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00506; -; 1.
InterPro; IPR001848; Ribosomal_S10.
InterPro; IPR005731; Ribosomal_S10_b.
Pfam; PF00338; Ribosomal_S10; 1.
PRINTS; PR00971; RIBOSOMALS10.
ProDom; PD001272; Ribosomal_S10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).
-!- FUNCTION: Involved in the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                              SEQUENCE FROM N.A.

MEDLINE=90163565; PubMed=2623943;

MEDLINE=90163565; PubMed=2623943;

McClory R.S., Cavanagh H.M.A.;

Spibey N., McClory R.S., Cavanagh equence of canine adenovirus types 1 and 2.";

Virus Res. 14:241-256(1989).
                                                                                                                                                                                                                                               Early ElA 20 kDa protein.
Canine adenovirus type 2.
Viruses; dsDNA viruses, n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                   NCBI_TaxID=10514;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR01049; rpsJ_bact; 1.
PROSITE; PS00361; RIBOSOMAL_S10; 1.
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Transcription regulation; SEQUENCE 171 AA; 18942
                                            PIR; B60010; B60010
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11541 MW; EF5AA895BBF63DCA
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Fusobacterales; Fusobacteriaceae;
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MW; 2
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                                                                                                                                                                                                                                                                                                                    annotation
                                                                                                                                                                                                                                                                                                                                         sequence update)
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Pred. No. 2.9;
2; Mismatches
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2527EC1338062FB0 CRC64;
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                                                                                                                                                                                                                                                   Adenoviridae; Mastadenovirus.
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MBL outstation -
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RESULT 12
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Best Local S
Matches 9
                                                               SMART; SM00051; DSL; 1.
SMART; SM00181; EGF; 2.
PROSITE; PS00022; EGF 1; 2
PROSITE; PS01186; EGF 2; 2
PROSITE; PS50026; EGF 3; 2
Differentiation; Repeat; T.
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01-NOV-1995
01-NOV-1995
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Bemis G., Wohldmann P.,
Submitted (MAR-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tax F.E., Yeargers J.J., Thomas J.H., "Sequence of C. elegans lag-2 reveals a with Delta and Serrate of Drosophila.", Nature 368:150-154(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2001) to -!- FUNCTION: PUTATIVE I
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LAG-2 OR LET-461 OR Y73C8B.4.
                                                                                                                                                                                               InterPro; IPR001774; DSL
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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MEDLINE=94187845; PubMed=8139658;
MEDLINE=94187845; PubMed=8139658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003
                      Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                        EMBL; X77495; CAA54629.1; -.
EMBL; AC024205; AAF36047.1;
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                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane DOMAIN: The DSL domain is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor.
SIMILARITY: Contains 2 EGF-like domains.
SIMILARITY: Contains 1 DSL domain.
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S42367; S42367.
V73C8B.4; CE22970.
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9; Conserv
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(Rel. 32,
(Rel. 41,
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                                                                  ; 2.
; 2.
; Transmembrane; ]
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Pred. No.
  POTENTIAL.
LAG-2 PROTEIN.
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RESULT 13
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Best Local S
Matches 7
TICE; TP0188; -; 1.
HAMAP; MF 00508; -; 1.
InterPro; IPR001848; Ribosomal S10.
InterPro; IPR005731; Ribosomal S10 b.
InterPro; IPR005731; Ribosomal S10; I.
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                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        spirochete.";
Science 281:375-388(1998).
-i- FUNCTION: Involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback Khalak H., Artiach P., Bowman C., Cotton M.D., Fujii C., Garlan McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garlan
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                                                                                               EMBL; AE001202; AAC65173.1; PIR; F71354; F71354.
                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the S10P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Treponema pallidum,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hatch B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum.
Bacteria; Spirochaetes;
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(Rel. 37, Last sequence up
(Rel. 41, Last annotation
al protein S10.
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                                                                                                                                                                                                                                                                                                                                          the binding
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EGF-LIKE 1.

EGF-LIKE 2.

EY SIMILARITY.

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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sandusky M.,
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arback T.,
., Garland S.,
Smith H.O.,
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RESULT 14
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Best Local S
Matches 8
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16-0CT-2001
16-0CT-2001
28-FEB-2003
  Hydrolase;
SIGNAL
PROPED
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ACT_SITE
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Trimeresurus gramineus (Indian green tree viper) (Green habu Trimeresurus gramineus (Indian green tree viper) (Green habu Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleost
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PRODOM; PD001272; RiBosomal_S10; 1.
TIGREAMS; TIGR01049; TABOSOMAL_S10; 1.
PROSITE; PS00361; RIBOSOMAL_S10; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 102 AA; 11584 MW; 2C7361
                                                                                                 PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SMO0020; TRYP SPC; 1.
PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                               InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Thrombin-like snake venom serine protease.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                     proteases."
FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deshimaru M., Oga
Shimohigashi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lepidosauria; Squamata; Scleroglossa
Viperidae; Crotalinae; Trimeresurus.
NCBI —
TaxID=8767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohno M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom gland;
MEDLINE=97096898; PubMed=8941719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                MEROPS; S01.185;
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Accelerated evolution of crotalinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRIGA
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Y., Fukumaki Y., Niwa M., Yamashina I
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                                                                                                                                                                                                                                          BAA19983.1; -.
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40, Last sequence upd
1. 41, Last annotation v
oteinase 3 precursor (EV
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53.3%;
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS01264; TBOX_2; 1.

PROSITE; PS50252; TBOX_3; 1.

Developmental protein; Transcription regulation; DNA-binding; Nuclear protein; Activator.

DNA_BIND 50 20 TBOX.

SEQUENCE 434 AA; 46714 MW; AAA50ZDA838D0A06 CRC64;
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Search completed: March 22, 2004; 06:53:02 Job time: 0.728738 secs

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9 caenorhabdi
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O92502 bombyx mori	092502	12	115	۲	<b>4</b> 4 57	40
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8	Q8SYK2	ហ	1324	43.1	47	ü
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Q8i511 plasmodium	Q8I511	υı	894	43.1	47	
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human	Q80AC1	12	841	43.1	47	29
human	Q80AC3	12	841	ω	47	28
1 human	Q98VL1	12	841	ω	47	27
human	Q9DX81	12	841	w.	47	26
$\vdash$	C9DWY1	12	841	ω.	47	25
Q8t5c4 aedes aegyp	Q8T5C4	ហ	486	ω.	47	
Q9ard1 lycopersico	Q9ARD1	10	290	ω.	47	23
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human t-	056228	15	4	ŗ	49	
Q9qra1 human t-lym	Q9QRA1	15	1273		49	
	Q8MRG9	ψı	796		49	
-	Q9VTR4	ຫ	796	45.0	49	18
O56227 human t-lym	056227	15	651		49	17

# ALIGNMENTS

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RESULT 1
Q9U6R7
                                                                  Weber E.R., Hunter S., Stedman K., McCall C.;

""Cloning and Characterization of a 98 kDa Allergen from
Permatophagoides farinae.";

RI Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

REMEL; AF178772; AAD52672.1; -.

REGO; GO:0005576; C:extracellular; IEA.

RGO; GO:00005975; F:chitth binding; IEA.

RGO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

RGO; GO:0005975; P:carbohydrate metabolism; IEA.

RGO; GO:0005975; P:chitth metabolism; IEA.

RGO; GO:0005975; P:chitth metabolism; IEA.

RGO; GO:0005975; Chitin bind PerA.

InterPro; IPR002557; Chitin bind PerA.

InterPro; IPR002557; Chitin bind PerA.

RINterPro; IPR00123; Glyco hydro 188.

RF InterPro; IPR001579; Glyco hydro 188.

RF Fam; PF00704; Glyco hydro 18; 1.

PF000m; PD000471; Glyco hydro 18; 1.

RRART; SM00636; Glyco 18; 1.

RRART; SM00636; Glyco 18; 1.

RGO; CO:000595; CHITNASE 18; 1.
Query Match
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Matches 18
                                                                Glycosidase; Hydrolase.
SEQUENCE 555 AA; 632
                                                                                                                                                                                                                                                                                                                                                                                                                                           Dermatophagoides farinae (House-dust mite).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Ana
Pyroglyphidae; Dermatophagoides.
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01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
98kDa HDM allergen.
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18; Conserv
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   Conservative
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                                                              63238 MW; 0E4564A1A459B30B CRC64;
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Score 103; DB 5;
Pred. No. 1e-08;
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InterPro; IPR00123; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18AS.
Pfam; PF01607; CBM 14; 3.
Pfam; PF00704; Glyco hydro 18; 3.
ProDom; PD000471; Glyco hydro 18; 3.
SMART; SM00494; ChtBD2; 3.
SMART; SM00494; Glyco 18; 3.
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PIR; T14075; T14075.
GO; GO:0005576; C:ext:
GO; GO:000861; F:chi
GO; GO:0008843; F:end
GO; GO:0016798; F:hyd
GO; GO:0005975; P:cazi
GO; GO:0006032; P:chi
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MEDLINE=9834849; PubMed=9662472;
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MEDLINE=9834849; PubMed=9662472;
MEDLINE=9834849; PubMed=9662472;
MEDLINE=9834849; PubMed=9662472;
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
NCBI_TaxID=7159;
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01-JAN-1998 (TrEMBLrel. 05, Last set:
01-CCT-2003 (TrEMBLrel. 25, Last and
Probable chitinase 2 (EC 3.2.1.14).
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GO:0008661; F:chitin binding; IEA.
GO:0008843; F:endochitinase activity; IEA.
GO:0016798; F:hydrolase activity, acting on
GO:0005975; P:carbohydrate metabolism; IEA.
GO:0006032; P:chitin catabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ect Mol. Biol. 7:233-239(1998).
CATALYTIC ACTIVITY: HYDROLYSIS
ACETYL-D-GLUCOSAMINE POLYMERS C
SIMILARITY: BELONGS TO CHITINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROLASES).
L; AF026492; AAB81850.1;
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Metazoa; Arthropoda; Hexap
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POLYMERS OF CHITIN
CHITINASE CLASS
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Pred. No. 2.5;
5; Mismatches
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Submitted
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Q9XFJ4;
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, 0
01-NOV-1999 (TrEMBLrel. 25, 1
01-OCT-2003 (TrEMBLrel. 25, 1
Calcium/calmodulin-dependent
CCAMK, OR CCAMK-2.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase act
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:protein amino acid phosphorylation;
InterPro; IPR002048; EF-hand.
InterPro; IPR002125; Recoverin.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
                                                                                                                                                                                   Prodom; FUDUNCA, 157; 3.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00110; PROTEIN_KINASE_DCM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00036; efhand; 3.
Pfam; PF00069; pkinsee; 1.
PRINTS; PR00450; RECOVERIN.
ProDom; PD000012; EF-hand; 1.
ProDom; PD000001; Prot_kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Mol. Biol. 0:0-0(1998).

-- SIMILARITY: BELONGS TO THE

EMBL; U38446; AAF21450.1; --

EMBL; AF087813; AAD52092.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CV. XANTHI;
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Liu Z., Poovaiah B
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CCAMK OR CCAMK-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. XANTHI; TISSUE=Anther;
Liu Z.H., Xia M., Poovaiah B.W.;
"Chimeric calcium/calmodulin-dependent protein kinase in tobacco:differential regulation by calmodulin isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Regulated expression of an anther-specific calcium/calmodulin dependent protein kinase causes male sterility in plant."; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                                  Similarity
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                                                 PHPTNIHKYLVCESVNG 19
PHPNVIHLYDVCEDPSG
                                                                                                         Conservative
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  113
                                                                                                      Score 55; DB 1
Pred. No. 1.1;
1; Mismatches
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                                                                                                                                                             Length
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Last sequence update)
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t protein kinase.

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517 A

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R PISH,
R Pfam; PF00069; pkinase; ...
R Pfam; PF00069; pkinase; 1.

PR PRINTS; PR00450; RECOVERIN.

PR PRODOM; PD0000012; EF-hand; 1.

PR PRODOM; PD0000012; FF-hand; 1.

PR PROST; SM00054; EFH; 3.

PR SMART; SM00054; EFH; 3.

PR SMART; SM000220; S TKC; 1.

DR PROSITE; PS00018; FF TEN KINASE DOW; 1.

PROSITE; PS000108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.
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Matches 10
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TEQUILA OR CG4821 OR CG4948 OR CG18403.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005529; F:calcium ion binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity;
GO; GO:0006740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR002048; EF-hand.
InterPro; IPR0001125; Recoverin.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                            Q8TOI5;
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SEQUENCE
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                                                                                                                                                                                                                                  01-JUN-2002
01-OCT-2003
                                                                                                                                                                                                                                                               01-JUN-2002
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                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00036; efhand; Pfam; PF00069; pkinase;
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                                                                                                                                                                                                                                                                                             PRELIMINARY;
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25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                        Brachycera; Muscomorpha;
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nisoforms.
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                                                                                                                                                                      Insecta; Pterygota;
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L C.J.,
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RESULT
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RA Addams M.D., Celniker S.E., Holt R.A., Shiturner M., Henderson S.N.,
RA George R.A., Lewis S.E., Holt R.A., Shahurner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Harli J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bernan B.P., Bhandari D., Bolshakov S.,
RA Ballew R.M., Basu A., Bernan B.P., Bhandari D., Bothier P.,
RA Burtis K.C., Bennan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dudson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Degwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shie B., Shen H., Shong T., Weinstock G.M., Wisskern D.R.,
Shen H., Woodeng T., Worther E., Wang S., Yao Q.A.,
Shen J., Y
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Best Local
Ye J., 1-
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NCBI_TaxID=7227;
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Pfam; PF01607; CBM_14; 5.
SMART; SM00494; ChtBD2; 5.
SEQUENCE 437 AA; 49481 MW; 1D2D73E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0023479; Tequila.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin bindin; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
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Drosophila melanogaster
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8; Conserva
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(TrEMBLrel.
(TrEMBLrel.
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(Fruit
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22,
25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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fly).
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PRUX PURPLE PROPERTY 
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Best Local (
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Q9BI19;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu I., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.I., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Evans C.A.,
                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
GRAAL2 protein precursor
TEQUILA OR GRAAL OR CG4821 OR CG4948 OR CG18403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO02557; Chitin_bind_
Pfam; PF01607; CBM 14; 7.
SMART; SM00494; ChtBD2; 7.
SEQUENCE 563 AA; 61963 MW; 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003553; AAF50322.2; -
FlyBase; FBgn0023479; Tequila.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008661; F:chitin binding; IEA.
GO; GO:0006630; P:chitin metabolism; I
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                                                                                   Drosophila melanogaster (Fruit fly),
Eukaryota; Metazoa; Arthropoda; Haspoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2002)
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Adams M.D., Celniker
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                                                     NCBI_TaxID=7227;
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHPHDVHKYLRC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHPTNIHKYLVC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Amanatides P.G., Brandon R.C.
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e EMBL/GenBank/DDBJ databases
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Pred. No. 1.8;
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                                                                                                                      Muscomorpha;
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                                                                                                                                                 Pterygota;
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RESULT
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REMBLY AJJOSOUS; CACSSZOS: 1: -.

R FLYBBBS; PRO750; IRTF.

R FLYBBBS; FEBGN0023479; Tequila.

R GG; GG:0005576; C:extracellular; IEA.

R GG; GG:0005576; C:extracellular; IEA.

R GG; GG:0005061; F:chitin binding; IEA.

R GG; GG:0008061; F:chimotrypsin activity; IEA.

R GG; GG:000823; F:peptidase activity; IEA.

R GG; GG:000823; F:crypsin activity; IEA.

R GG; GG:0006295; F:trypsin activity; IEA.

R GG; GG:0006508; F:proteclysis and peptidolysis; IEA.

R GG; GG:0006508; F:proteclysis and peptidolysis; IEA.

R GG; GG:0006508; F:proteclysis and peptidolysis; IEA.

R GG; GG:0006508; F:proteclysis and PerA.

InterPro; IPR002557; Chitin bind PerA.

InterPro; IPR002172; LDL receptor A.

InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001190; Srcr_receptor.

R InterPro; IPR001191; Srcr_receptor.

R Pfam; PF01007; IAC recept_a; 2.

Pfam; PF00057; IAC recept_a; 2.
                                                                                                                                                                                                                                                                                                                                            Matches
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PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00251; LDLRECEPTOR.

PRINTS; PR00251; SPERACTRCPTR.

SMART; SM00494; ChtBD2; 15.

SMART; SM00192; LDLa; 2.

SMART; SM00202; SR; 2.

SMART; SM00202; Tryp_SPc; 1.

PR051TE; PS01209; LDLRA 1; 1.

PROSITE; PS0068; LDLRA 2; 2.

PROSITE; PS00420; SRCR_1; 2.

PROSITE; PS00420; SRCR_1; 2.

PROSITE; PS00420; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Munier A.I., Medzh
                                                                                                                                                      Q9VSU2; Q9VSU1;
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                    TEQUILA OR CG4821 OR CG4948 OR CG18403.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Beukaryota, Metazoa; Arthropoda; Brachycera; Muscomorpha;
Rephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
SEQUENCE FROM N.A.
STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                         CG4821 protein.
                                                                                                                                                                                                                 Q9VSU2
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                                                   NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Protease;
                                                                                                                                                                                                                                                                                                                                                                                                  2382 AA;
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                        49.5%;
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Last annotation update)
                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                           Score 54; DB 5;
Pred. No. 8.2;
2; Mismatches
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                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    51C85282B06833D4 CRC64;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfelffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Blazen D.A., Bucller H., Cadleu E., Center A., Chandra I.,
RA Gebablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattel B., McIntosh T.C., Willey M.M., Glasser X.,
RA Harris N.L., Mattel B., McIntosh T.C., Willey D., Lai Z.,
RA Liuk X., Mattel B., McIntosh T.C., Willey M.P., McPherson D.,
RA Wount S.M., Noy M., Murphy B., Murphy L., Murphy R., Smith T.,
RA Melson D.R., Nelson K.A., Standers R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Standers R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Standers R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Standers R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Standers R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Singson M., Stupski M.P., Smith T.,
RA Melson D.R., Shen B., Shen H., Shen B.,
RA Melson D.R., Shen B., Shen H., Shen B.,
RA Melson D.R., Shen B., Shen M., Shen B.,
RA Melson D.R., Shen 
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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

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A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson M., Moy M.,
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Smith C.D.,
niker S.E.,
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Best Local S
Matches 8
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SMART; SM00202; TRYP SPC; 1.

SMART; SM00020; TRYP SPC; 1.

PROSITE; PS00152; ATPASE ALPHA BETA; 1.

PROSITE; PS01209; LDLRA 1; 1.

PROSITE; PS00400; SRCR 1; 2.

PROSITE; PS00420; SRCR 2; 2.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50240; TRYPSIN_BER; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 2786 AA; 308362 MW; 2EED7A
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Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00251; LDLRECEPTOR.

PRINTS; PR00258; SPERACTROPTR.

SMART; SM00494; ChtBD2; 15.

SMART; SM00494; ChtBD2; LDLa; 2.

SMART; SM00192; SR; 2.
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GO; GO:0005576; C:extracellular;
GO; GO:00016020; C:membrane; IEA.
GO; GO:0005524; F:AlTP binding; II
GO; GO:0005524; F:chitin binding; II
GO; GO:000861; F:chitin binding
GO; GO:0008233; F:peptidase activit
GO; GO:0008234; F:scavenger rece
GO; GO:0005044; F:scavenger rece
GO; GO:0006030; F:trypsin activit
GO; GO:0006030; P:proteolysis an
GO; GO:0006508; P:proteon transpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           003967;
01-JUL-1997
01-JUL-1997
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Bacteriophage phigle.
Viruses; dsDNA viruses,
NCBI_TaxID=52979;
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HSSP; P00750; 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             003967
                                                                                                                               MEDLINE=97225795; PubMed=9073065;
Kodaira K.I., Oki M., Kakikawa M.
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O; GO:0016020; C:membrane; IEA.
O; GO:0016020; C:membrane; IEA.
O; GO:0005524; F:chitin binding; IO;
O; GO:0008261; F:chitin binding;
O; GO:0004263; F:chymotrypsin activity
O; GO:0005294; F:scavenger receptual Go:0005044; F:scavenger receptual Go:0006295; F:trypsin activity
O; GO:0006295; F:trypsin activity
O; GO:0006095; F:proteolysis and J;
O; GO:0006099; P:proteolysis and J;
O; GO:0015992; P:proteon transport
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rPro; IPR001190; 9
; PF01607; CBM_14
; PF00057; ldl_re
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8; Conserv
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0015992; P:proteon transport; IEA.
0; IPR000194; ATPase abcentre.
0; IPR002557; Chitin_bind_PerA.
0; IPR002172; LDL receptor_A.
0; IPR001254; Peptidase_S1.
0; IPR001314; Peptidase_S1A.
0; IPR001199; Srcr_receptor.
0; IPR001199; Srcr_receptor.
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F:scavenger receptor activity;
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_recept_a; 2.
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PEPTIDASE FAMILY S1.
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Last
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Pred. No. 9.7;
2; Mismatches
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InterPro; IPR001223; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18.
InterPro; IPR001579; Glyco hydro 18AS.
Pfam; PF01607; CBM 14; 1.
Pfam; PF00704; Glyco hydro 18; 1.
ProDom; PD000471; Glyco hydro 18; 1.
SMART; SM00494; ChtBD; 1.
SMART; SM00495; CHITINASE 18; 1.
PROSITE; PS01095; CHITINASE 18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998
01-JUN-1998
01-OCT-2003
  Q21139;
Q21139;
01-NOV-1996
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF008575; AAB87764.1; -.
PIR; T44445; T44445.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:0008061; F:hydrolase activity, acting on GO; GO:0008975; P:carbohydrate metabolism; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Shen Z., Jacobs-Lorena M.,"
"Characterization of a novel gut-specific human malaria vector Anopheles gambiae.",
J. Biol. Chem. 272:28895-28900(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Ano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1995) to th
EMBL; X98106; CAA66757.1;
EMBL; X90510; CAA62091.1;
SEQUENCE 66 AA; 7557 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  044079
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[2]
                                                                                                                                                                                                                                                                                                                                                Glycosidase; Hydrolase.
SEQUENCE 525 AA; 57211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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9; Conserv
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  (TrEMBLrel. 01, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                Conservative
                                                                  PRELIMINARY;
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Last annotation update)
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                                                                                                                                                                                                                                                              Score 53; DB
Pred. No. 2.4;
3; Mismatches
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4; Mismatches
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Best Local S
Matches
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PIR; T16525; T16525.

WORMPep; K02E10.8; CE33930.

InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig.
Pfam; PF000479; Ig. 4.

SMART; SM00409; IG. 4.

SMART; SM00408; IGC2; 4.

PROSTIB; PS50835; IG LIKE; 5.

SEQUENCE 727 AA; 80863 MW;
[2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R., Wams]
Waterston R., Wams]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8MNX4;
01-OCT-2002
01-OCT-2002
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STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
Submitted (MAY-2003)
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STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical T11F1.7.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                     "Genome sequence of the nematode investigating biology. The C. elections 282:2012-2018(1998).
                                                                                                                                                                                                                                                    Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                      ICBI_TaxID=6239;
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Wamsley P.; of C. elegans
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EMBL/GenBank/DDBJ databases.
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Pred. No.
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Mismatches
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      T11F1.";
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D Q94DE8

PREDITION

D Q94DE8;

AC Q94DE8;

DT 01-DEC-2001 (TERMBLrel. 19, Created)

DT 01-DEC-2001 (TERMBLrel. 25, Last sequence update)

DT 01-DEC-2003 (TERMBLrel. 25, Last annotation update)

DT 01-DEC-2003 (TERMBLrel. 25, Last annotation update)

DE P0683F02.4 protein (OJ1402 H07.12 protein).

GN P0683F02.4 OR OJ1402 H07.12.

GN P0683F02.4 OR OJ1402 H07.12.

OS Oryza sativa (Rice), and

OS Oryza sativa (Japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tochartojhyta; Magnoliophyta; Liliopsida; Poales; Poar CEhrhartoideae; Oryzaae; Oryza.

OC Ehrhartoideae; Oryzaa.
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ID Q94DE

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Q9VR79
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  Q9VR79
Q9VR79;
01-MAY-2000
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PROSITE;
SEQUENCE
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GO; GO:0005006; F:epidermal growth
InterPro; IPR000494; EGFR L domain.
Pfam; PF01030; Recep L domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL, AP003289; BABG3701.1; -.
EMBL, AP003415; BAC03323.1; -.
Gramene; Q94DE8; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=O. sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
clone:P0683F02.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. SPECIES=O.sativa;
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                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001064; Crystallin.
InterPro; IPR001159; DS RBD.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA;
PROSITE; PS50137; DS RBD; 1.
SEQUENCE 721 AA; 80021 MW; 6A004326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone:0J1402_H07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005622; C:intracellular; 1
GO:0003725; F:double-stranded
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523 AA; (
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       (TrEMBLrel.
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noto T., Yamamoto K.;
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Pred. No. 5.3;
2; Mismatches
    Created)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA binding;
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       RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F., RA Amanatides P.G., Jewis S.E., Richards S. Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Buttis K.C., Busen D.A., An H.-J., Andrews-Pfankoch C., Baldwin D., RA Burtis K.C., Busen D.A., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busen D.A., Butler H., Cadleu E., Cener A., Dovies P. RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Broxengor L.B., Davies P. RA Bodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunis P. Golson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunis P. Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Libeywam C., Liu Z., Marking J., Levitsky A.A., Li J., Li Z., Kulp D., Liai Z., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Smith T., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Mennett K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Nelson D.R., Walthing A.C., Stapleon M., Skupski M.P., Smith T., Ra Palazzolo M., Walthing A.C., Stapleon M., Skupski M.P., Smith T., Ra Palazzolo M., Walthing A.C., Stapleon M., Skupski M.P., Smith T., Ra Palazzolo M., Stong F.N., Zhong K., Zhong G., Zhoo Q., Zheng L., Theng G., Zhoo Q., Zheng L., Theng G., Zhoo Q., Zheng L., Theng G., Zhoo 
                                                                                                              Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., A Banzon J.W., Center A., Champe M., Davemport L.B., Dietz S.M., A Carlson J.W., Center A., Champe M., Davemport L.B., Dietz S.M., A Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D., A Ferriera S., Frise E., Galle R.F., Gary N.S., George R.A., A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smikhs R., Venter J.C., Rubin G.M., "Sequencing of Drosophila melanogaster genome.";

"Sequencing of Drosophila melanogaster genome.";
  SEQUENCE FROM N.A. Misra S., Crosby M. Hradecky P., Huang Y Tupy J.L., Bergman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22
01-OCT-2003 (TrEMBLrel. 25
CG17052 protein (LD43683p)
CG17052.
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MEDLINE=20196006; PubMed=10731132;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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  OKA
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  Matthews B.B., Bay:
Kaminker J.S., Pro-
Berman B., Carlson
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annotation
Bayraktaroglu L., Car
Prochnik S.E., Smith
lson J.W., Celniker S
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K.A.,

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K.A., Nunco J.,

Campbell ith C.D., r S.E.,

Holt R.A.,

Zheng L., Smith H.O.,

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PRESULT

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                                                      PROUBNCE FROM N.A.

A Varatharajalu V., Kubofcik J., Williams S.A., Kal A Varatharajalu V., Kubofcik J., Williams S.A., Kal A Varatharajalu V., Kutman T.;

"Molecular characterization of endochitinase from microfilarial cDNA library.";

microfilarial cDNA library.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ dat R. Co., GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0006031; F:hydrolase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0006030; P:chitin metabolism; IEA.

R. GO; GO:0006030; P:chitin bind PerA.

InterPro; IPR0012557; Chitin bind PerA.

InterPro; IPR001253; Glyco_hydro_18AS.
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Best Local 9
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EMBL; AB003572; AAF50927.2; -.
EMBL; BT001512; AAN71267.1; -.
FlyBase; FBBR0031097; CG17052.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:0008061; F:chitin metabolism; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
InterPro; IFR003557; Chitin_bind_PerA.
Pfam; PF01607; CBM 14; 3.
EMART; SM00494; ChiBD2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorestt V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Adams M.D., Celniker S.E., C
Submitted (MAR-2000) to the
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Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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01-OCT-2000
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Celniker S.,
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(TrEMBLrel. 25, Last annotation update)
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Search completed: March 22, 2004, 06:59:22 Job time: 4.82324 secs

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#### ALIGNMENTS

#### RESULT 1 PAYS2520 ID AAY5 XX AAY5 XX AAY5 XX AAY5 XX AAY5 XX AAY5 XX Mite XX M Mite allergen protein; map; high molecular weight; HMM-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation. AAY52520 standard; peptide; 19 Dermatophagoides farinae. House dust mite allergen protein (map) A/B fragment map(10) 22-FEB-2000 16-APR-1,999; 28-OCT-1999 WO9954349-A2 (first entry) 99WO-US008524.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.

Claim 3; Page 70; 154pp; English.

Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWM -map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. The HMW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines,

ABB47881 ABP97893

Soybean 3 Novel hum

Listeria Drosophil Drosophil

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Drosophil
Anopheles

AAY52535 AAU96339 AAY52533 AAU96337 AAU96338 AAO17674 AAO17673 ABP33819 AAW30919 AAW30919

AAU96329 AAY52523

AAY52525

AAU96327 AAU96328

Aau96328

Der HMW-m

WPI; 2000-052700/04.

Mccall

Hunter SW,

Weber 뗥;

(HESK-) HESKA CORP. Ç

HMW-m

House dus Der HMW-m

Der HMW-m Der HMW-m

dus

17-APR-1998; 13-MAY-1998; 02-SEP-1998;

98US-00062013. 98US-0085295P. 98US-0098909P.

House dus

D. pteron Der HMW-m

D. pteron Der HMW-m

B tropica B tropica Human ORF

AAU96324 AAY52512

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100.0%;
Score 109;
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Query Match Best Local S Matches 19

Local Similarity

100.0%;

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X និនិនិនិនិនិនិ 문 Ś Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a nongroup proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the catherapeutic of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a classe. Antibodies that bind to Der HMW-map ac useful for inhibiting chinding of proteins to IgE, to prevent immunocomplex formation, thus creducing hypersensitivity responses to mite allergens, and as vaccines capainst mite allergen hypersensitivity. Sequences ANU96314-AAU96342 Query Match Best Local S Matches 19 humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite mite allergenic protein; immunocomplex formation. Sequence 19 AA; Der HMW-map; American house mite allergenic protein; imm AAU96324; AAU96324 standard; allergens from a The invention relates to an isolated mite allergenic protein of New mite allergenic protein isolated from Dermatophagoides, designa Der HMW-map protein, useful as a vaccine for treating mite allergy. Mccall 14-SEP-2000; 2000US-00662293 14-SEP-2001; 2001WO-US028730 21-MAR-2002 WO200222807-A2 Dermatophagoides farinae Der HMW-map polypeptide #11 WPI; 2002-351888/38 15-JUL-2002 (HESK-) HESKA CORP 19; Ç Similarity DIPHPTNIHKYLVCESVNG 19 DIPHPINIHKYLVCESVNG 19 Conservative Hunter SW, (first entry) 71; 161pp; mixture of proteins peptide; 19 100.0%; Weber ise dust mite; antiallergic; mite; IgE; immunoglobulin E; hypersensitivity; English. 0 Score 109; DB 3; Pred. No. 2.6e-11; ; Mismatches 0; Ħ A Length 19; Indels <u>.</u> designated Gaps 0

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                                                                         mapB (98 kD). Mice allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunites animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen map composition. The HMW-map composition was isolated from the composition was isolated from the composition with the composition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -map) composition. The HMW-map composition was isolated from a D. fa homogenate by gel filtration, with each fraction being analysed for presence of proteins that bound to IgE present in mite-allergic dog antisera. The HMW-map composition comprises mapA (a 109 kD protein)
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mite allergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Der HMW-map;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Der HMW-map polypeptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU96316 standard; peptide;
                                                                  22-FEB-2000
                                                                                                                              AAY52525;
                                                                                                                                                                                    AAY52525 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mite allergenic protein isolated from Dermatophagoides, designa HYW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                   DIPHPTNIHKYLVCESVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                             DIPHPTNIHKYLVCESVNG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             American house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erican house dust mite; antiallergic; mite; IgE;
protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weber
                                                                                                                                                                                    536
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                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109; DB 5;
Pred. No. 2.8e-11;
                                                                                                                                                                                        ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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AAU96329 standard; protein; 536 AA

AAU96329; 15-JUL-2002 Der HMW-map

polypeptide #16

(first entry)

Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.

음 성

493

DIPHPINIHKYLVCEFVNG 511

1 DIPHPTNIHKYLVCESVNG 19

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This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-536, the mature form of PDerf98-556 (AAY5523). PDerf98-536 CC has a molecular weight of 98 kD, comprising 536 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite component of the Dermatophagoides farinae high molecular weight mite component of the Dermatophagoides farinae high molecular weight mite component of the permatophagoides farinae high molecular weight mite consistence in partial composition was sold fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. Mite allergenic proteins and compositions to modify an animal's hypersensitivity reaction to mite compositions to modify an animal's hypersensitivity reaction to mite callergens. Animals that may be treated include mammals and birds, ceptially felines, canines, equines, humans, other pets, and work or composition and skin test. The proteins and peptides can also be used to callergies via a skin test. The proteins and peptides can also be used to craise antibodies, which have a variety of potential uses. For example, can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to crecover desired dust mite allergens from a mixture of proteins
                Query Match
Best Local S
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fel canine; veterinary; antibody; vaccine; immunisation.
                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-052700/04.
N-PSDB; AAZ38579, AAZ38580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 125-127; 154pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccall
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18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                    Similarity
                                                                              536 AA;
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00062013.
98US-0085295P.
98US-0098909P.
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                  94.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber
<u>,</u>
                  Score 103; DB 3;
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    묤,
    Mismatches
                                      Length 536;
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a nonprotein suseful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A composition is useful for desentifying an animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)s or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                  Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                             AAY52523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 125-127; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000; 2000US-00662293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-2001; 2001WO-US028730
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                                                Protein
                                                                                                                         Dermatophagoides farinae
                                                                                                                                                                                                                               House dust mite (D. farinae) mite allergen protein (map) PDerf98-555
                                                                                                                                                                                                                                                               22-FEB-2000
                                                                                                                                                                                                                                                                                                                         AAY52523 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mccall CA,
                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-351888/38
                                                                                                                                                                                                                                                                                                                                                                                                     493
                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIPHPINIHKYLVCESVNG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                     veterinary; antibody; vaccine; immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK69575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     DIPHPTNIHKYLVCEFVNG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑĀ.;
                                                                                                                                                                                                                                                               (first
                                               /note= "Signal peptide"
20. .555
                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.5%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 103; DB 5;
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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"Mature PDerf98-555"

14-SEP-2001; 2001WO-US028730

21-MAR-2002 WO200222807-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents Dermatophagoides farinae mite allergen protein (map) pDerf98-555. pDerf98-555 has a molecular weight of 98 kD, comprising 555 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWM-map) composition. The HWM-map composition was isolated from a D. farinae chomogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to 19E present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to read a winch have a correct fragments and uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allerges from a migrary of positive controls in test kits and as tools to recover desired dust mite
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578
                                                                                                 Dermatophagoides
                                                                                                                             mite allergenic protein; immunocomplex formation.
                                                                                                                                                Der HMW-map; American house dust mite; antiallergic; mite; I mite allergenic protein; immunoglobulin E; hypersensitivity.
                                                                                                                                                                                             Der HMW-map polypeptide #14
                                                                                                                                                                                                                               15-JUL-2002
                                                                                                                                                                                                                                                               AAU96327;
                                                                                                                                                                                                                                                                                               AAU96327 standard; protein; 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 111-113; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-052700/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mccall CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORP.
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98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.5%;
94.7%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 555
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                                                                                                                                                               IGE;
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14-SEP-2000; 2000US-00662293

HESKA CORP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
                             WPI; 2002-351888/38
N-PSDB; ABK69573.
                                                                                                         Mccall CA,
                                                                                                                                                                                                                           14-SEP-2000; 2000US-00662293
                                                                                                                                                                                                                                                                                   14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                                                                                                                              21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                   WO200222807-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dermatophagoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mite allergenic protein; immunoglobulin immunocomplex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Der HMW-map;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Der HMW-map polypeptide #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU96328 standard; protein; 555 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cat) susceptible to or having an allergic response to a mite. therapeutic composition is useful for desensitising a host and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 114-116; 161pp; English.
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Der HMW-map protein, useful as a vaccine for treating mite allergy.
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DB; ABK69571.
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                                                                                                            Hunter SW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          American house dust mite; antiallergic; mite; I nic protein; immunoglobulin E; hypersensitivity;
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                                                                                                               Weber ER
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Pred. No. 1.3e
0; Mismatches
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RESULT 10
AAY52535
ID AAY52535
AC AAY52
XX AAY52
XX DF 06-AU
DT 06-AU
DT 22-FE
XX Mite
KW Mite
KW house
KW woosi
KW canin
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Derma
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II-AI
PR 113-MI
PR 113-MI
PR 12-SI
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PA (HES)
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WPI
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                                                                                                                                     17-APR-1998;
13-MAY-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D. pteronyssius 98 kD mite allergen protein (map)
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22-FEB-2000
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                                                                   Mccall CA,
                                                                                                                                                                                                           16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                     Dermatophagoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                       canine; veterinary;
                                                                                                                                                                                                                                             28-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                  Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.5%;
(larity 94.7%;
Conservative
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(first entry)
                                                                                                       CORP
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                                                                                                                                    98US-00062013.
98US-0085295P.
98US-0098909P.
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                                                                                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                     action; therapy; treatment; diagnosis; human; feline;
antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                               "Asn is N-glycosylated"
                                                                     Weber
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Pred. No. 1.3e-08;
0; Mismatches 1
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0;

WPI; 2000-052700/04. N-PSDB; AAZ38589, AA

AAZ38590

Claim

3; Page 147-149; 154pp; English.

Nove1

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high molecular weight Dermatophagoides nucleic acid polypeptides to modify an animals' hypersensitivy to mite allergens.

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ARUSULT 11
AAU96339
ID AAU96
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XX M mite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dermatophagoides farinae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2001; 2001WO-US028730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Der HMW-map polypeptide #26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU96339 standard; protein; 490
                                The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its relat
                                                                                                                                                             New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                         144-146; 161pp;
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Pred. No. 0.00036;
4; Mismatches 1;
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                                                                                                         English.
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                                   its related nucleic
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This sequence protein (map)

represents Dermatophagoides pteronyssius mite allergen PDerp98-509, PDerp98-509 has a molecular weight of 98 i

Claim 3;

154pp;

English

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RESULT 12
AAY52533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mite allergen protein; map; high molecular weight; HYM-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; fel canine; veterinary; antibody; vaccine; immunisation.
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22-FEB-2000
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13-MAY-1998;
                                                                                                                                                                                                                                                                                                      28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                Dermatophagoides pteronyssinus
                                                                     Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                N-PSDB; AAZ38585,
                                                                                                                             WPI; 2000-052700/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; protein; 509
                                                                                                                                                       Hunter SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first en
                                                                                                                                                                                      CORP.
                                                                                                                                                                                                               98US-00062013.
98US-0085295P.
98US-0098909P.
                                                                                                                                                                                                                                                                          99WO-US008524
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                         note= "Signal peptide"
                                                                                                               AAZ38586, AAZ38587, AAZ38588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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Pred. No. 0.00036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; human; feline,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 490;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2001; 2001WO-US028730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 509
                                                                                                                                                                                                                                                                                                                                                        Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mccall CA, Hunter SW,
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                                                                                                                                                                                                                                                                                                                                                                                                                        HMW-map
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mite allergenic
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                                                                                                                                                                                                                                                                                                                                                    Page 134-136; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        protein, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 0.
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les 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Dermatophagoides, designated for treating mite allergy.
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RESULT 14
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                                 The invention relates to an isolated mite allergenic protein of CD Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for elliciting an immune response egainst Der HMW-map protein. The protein or a reagent comprising a non-protein acceous epitope is useful for identifying an animal (e.g., dog, cat) succeptible to or having an allergic response to a mite. An expendition is useful for desensitising a host animal to an the animal to a succeptible to a mite. The DNA and protein can be used in the CC detection of anti-Der HMW-map partial fluids, and inhibition confimmunoglobulin (19) or Der HMW-map protein activity associated with a clisease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to 19E, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 or represent Der HMW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
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Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WC200222807-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Der HMW-map; American house dust mite; antiallergic; mite; l
mite allergenic protein; immunoglobulin E; hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 139-141; 161pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-351888/38
N-PSDB; ABK69583.
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61.9%;
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No. 0.
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Query Match

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RESULT 15
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to isolated protein allergens from the Blomia tropicalis mite, designated Blot 3 and Blot 12(8). The protein allergens are useful for preventing, reducing or ameliorating a B. tropicalis hypersensitivity condition, such as asthma, atopic dermatitis or rhinitis. The present sequence is a protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New protein allergens from the mite Blomia tropicalis, useful as vaccine for preventing, reducing or ameliorating a B. tropicalis hypersensitivity or allergic conditions, e.g. asthma, atopic dermatitis or rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mite; allergen; Blot 3; Blot 12(S); Blot 12; dust mite; immunisation; antiallergic; anti-inflammatory; immunomodulatory; storage mite; asthma; atopic dermatitis; rhinitis; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 143 AA;
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N-PSDB; AAL46687.
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13-OCT-2000; 2000AU-00000731.
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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Query
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|: /cgn2_6/ptodata/2/pubpaa
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/ Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
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US-10-425-114-69228	US-10-424-599-260414	US-10-424-599-232599	US-10-222-723-17	US-10-424-599-260412	US-10-424-599-272856	US-09-864-408A-5584	US-10-218-743-38	US-10-218-743-35	US-10-218-743-41	US-10-218-743-18	US-10-218-743-15	US-10-218-743-21	US-10-218-743-3	US-10-218-743-11	ID
Sequence 69228, A	Sequence 260414,	Sequence 232599,	Sequence 17, Appl	Sequence 260412,	272856	82	Sequence 38, Appl	ა 5	41,	18,	15,	Sequence 21, Appl	w -	Sequence 11, Appl	Description

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DIPHPTNIHKYLVCESVNG 19

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Sequence 144132,	<u></u>	ø	ω	e 10, App	o	e 3871	1124, A	212	26378	Sequence 131, App	(A)	Sequence 277795,	(I) 	Sequence 18401, A	o.	ω	o o	(D UT	e 7	ரு ப	ហ	Sequence 144566,	on on	2747	5522	:55, App	114	ce 18,	

#### ALIGNMENTS

RESULT 1 US-10-218-743-11

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FILE OF INVENTION.
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
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                                                                                                                                                                                                  ; LENGTH; 19
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-11
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Publication No. US20030096779A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Mu
APPLICANT: Weber, Eric R.
APPLICANT: MCDERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                     Matches
                                                                                                                                          Query Match
                                                                               'Match 100.0%; Score 109; DB 14;
Local Similarity 100.0%; Pred. No. 7.5e-10;
Les 19; Conservative 0; Mismatches 0;
1 DIPHPTNIHKYLVCESVNG 19
                                                                                                                                       DB 14;
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; LENGTH: 20
TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-3
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PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR PILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098,295
PRIOR APPLICATION NUMBER: 60/098,525
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
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PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/218,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McCall, Catherine A. APPLICANT: Hunter, Shirley Wu APPLICANT: Weber, Eric R.
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/062,013
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ORGANISM: Dermatophagoides farinae
                                                                                                                                                                                                                                                                       RAPPLICATION NUMBER: 60/098,909
FILING DATE: 1998-09-02
APPLICATION NUMBER: 60/085,295
FILING DATE: 1998-05-13
                                                                                                                                                                                                                     APPLICATION NUMBER: 60/098,565
FILING DATE: 1998-04-17
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Sequence 18, Application US/10218743

Publication No. US20030098779A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: AL-2-C3
CURRENT TRILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/085,295
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PRIOR FILING DATE: 1999-04-15
PRIOR PEPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
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SEQ ID NO 15
LENGTH: 555
TYPE: PRT
ORGANISM: Dermatophagoides farinae
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Best Local Similarity
Matches 18; Conserv
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Best Local !
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CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
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PRIOR APPLICATION NUMBER: 09/062,013
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APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
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APPLICATION NUMBER: 09/062,013 FILING DATE: 1998-04-17
                                                              FILING DATE: 1998-04-17
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94.7%;
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Pred. No. 2.1e-07
0; Mismatches
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Pred. No. 2.1e-07;
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US-10-218-743-41
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                                                  Sequence 35, App
Publication No.
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SEQ ID NO 41
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SEQ ID NO 18
LENGTH: 555
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                                                                                TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL2-C3 CURRENT APPLICATION NUMBER: US/10/218,743 CURRENT FILLING DATE: 2002-08-13 CURRENT FILLING DATE: 2002-08-13
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PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
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PRIOR APPLICATION NUMBER: 09/062,013
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PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
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PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
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PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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No. US20030096779A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.2%;
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US-09-864-408A-5584

Sequence 5584, Application US/09864408A Publication No. US20040009474A1 GENERAL INFORMATION:

APPLICANT: Leach, Martin D.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Enco

CURRENT APPLICATION NUMBER: US/09/864,408A

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US-10-218-743-38
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SEQ ID NO 35
LENGTH: 509
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IITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: AL-2-C3 USES THEREOF FILE REFERENCE: AL-2-C3 USES THEREOF FILE REFERENCE: AL-2-C3 USES THEREOF FILE REPERIOR: NUMBER: US/10/218,743 UCRRENT FILING DATE: 2002-08-13 PRIOR APPLICATION NUMBER: US/09/292,225 PRIOR FILING DATE: 1999-04-15 PRIOR FILING DATE: 1999-04-15 PRIOR APPLICATION NUMBER: 60/098,909 PRIOR FILING DATE: 1998-09-02 PRIOR APPLICATION NUMBER: 60/085,295 PRIOR APPLICATION NUMBER: 60/085,295 PRIOR APPLICATION NUMBER: 60/098,565 PRIOR APPLICATION NUMBER: 60/098,565 PRIOR APPLICATION NUMBER: 60/098,565 PRIOR FILING DATE: 1998-04-17 PRIOR APPLICATION NUMBER: 60/098,565 PRIOR FILING DATE: 1998-04-17 PRIOR APPLICATION NUMBER: 60/098,565 PRIOR FILING DATE: 1998-04-17 PRIOR PRIO
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PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
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                                                                                                                                                      Local Similarity
les 13; Conserv
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Local Similarity 61.9%;
464 LPHPTDVHKYLVCEYIATPNG 484
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                                                                                                                                                      Conservative
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61.9%;
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Pred. No. 0.0023;
                                                                                                                                                                                      Score 76.5;
Pred. No. 0.
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                                                                                                                                                                                              0023;
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                                                                                                                                                                                                                                  DB 14;
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RESULT 11
US-10-424-599-260412
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; CTHER INFORMATION: Clone ID:
US-10-424-599-272856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-864-408A-5584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                  Sequence 260412, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 272856, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5584
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 272856
LENGTH: 60
                                                                         SEQ ID NO 260412
LENGTH: 291
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                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                               TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE:
                                                                                                             NUMBER OF SEQ ID NOS: 285684
                     TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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OTHER INFORMATION: Clone ID: PAT_MRT3847_77175C.1.pep
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77.8%;
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Pred.
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Pred. No.
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-222-723-17
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US-10-222-723-17
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                                                                          US-10-424-599-232599
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SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
Matches
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Best Local Similarity
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Publication No.
                          Matches
                                      Best Local
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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APPLICANT: Saverio C. Falco
APPLICANT: Dennis Flint
APPLICANT: Dennis Flint
APPLICANT: Steven Gutteridge
TITLE OF INVENTION: 3-Deoxy-D-Manno-Octulosonic Acid 8-Phosphate Synthases
FILE REFERENCE: BB1512 USNA
TITLE OF INVENTION: 3-Deoxy-D-Manno-Octulosonic Acid 8-Phosphate Synthases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/222,723
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/312,679
PRIOR FILING DATE: 2001-08-16
                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_52061C.1.pep
                                                                                                 ORGANISM: Glycine max FEATURE:
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8; Conserv
                         Similarity 7; Conserv
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 HPTNIHKYLVCESV 17
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                          Conservative
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                                    42.2%;
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Pred. No. 4
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Pred. No. 44;
                                       Score 46; DB
Pred. No. 19;
                          Mismatches
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                                                 Length 95;
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                          Indels
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Sequence 5928, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Vihua
APPLICANT: Zhou, Yihua
APPLICANT: Zovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Papaska, Jack E
APPLICANT: Papaska, Jack E
APPLICANT: Papaska, Jack E
APPLICANT: Tabaska, Jack E
APLICANT: Tabaska, Jack E
APPLICANT: Tabaska
Sequence 560414, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
CAO YOUNGE
APPLICANT:
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42.2%; Score 46; DB 12; Length 156;
Best Local Similarity 47.1%; Pred. No. 32;
Matches 8; Conservative 5; Mismatches 4; Indels
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58.3%; Pred. No. 36;
ive 1; Mismatches 4; Indels
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) OTHER INFORMATION: Clone ID: UC-ZMFLMO17103F03_FLI.pep
US-10-425-114-69228
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CTHER INFORMATION: Clone ID: PAT_MRT3847_77177C.1.pep
US-10-424-599-260414
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88 DIPIVIDVHETIHCEAV 104
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Best Local Similarity 58.3
Matches 7; Conservative
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ORGANISM: Zea mays
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US-10-425-114-69228
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Search completed: March 22, 2004, 07:45:49 Job time: 3.8866 secs

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FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
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Sequence 21, Appl
Sequence 20, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 35, Ap
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Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 50, Appli
Sequence 4, Appli
Patent No. 545961
Sequence 1269, Ap
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Sequence 21, Appl
Sequence 8, Appli
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                                                                                       March 22, 2004, 06:42:54; Search time 1.53141 Seconds (without alignments) 640.518 Million cell updates/sec
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Sequence 18,
Sequence 41,
Sequence 35,
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-292-225-31
US-09-292-225-115
US-09-292-225-41
US-09-292-225-35
US-09-292-225-35
US-09-292-225-35
US-09-257-8258-20
US-09-257-8258-20
US-09-257-8258-20
US-08-33-7118-18
US-09-257-8258-35
US-09-257-8258-35
US-09-257-8258-35
US-09-328-352-5038
US-09-328-350-38
US-08-631-768A-1
US-08-631-768A-1
US-09-280-197-1
US-09-281-768A-1
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-292-225-11
US-09-292-225-3
                                                                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            - protein search, using sw model
                                                                                                                                                  US-09-662-293-11
109
1 DIPHPTNIHKYLVCESVNG 19
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                            Searched:
                                                                                           Run on:
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Sequence 8, Appli Sequence 6, Appli Sequence 8, Appli Sequence 2, Appli Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl Sequence 6599, Ap Sequence 6599, Ap Sequence 5599, Ap Sequence 10, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 25, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli	ACID MOLECULES, PROTEINS	Length 19; Indels 0; Gaps 0; ACID MOLECULES, PROTEINS
28 41 37.6 509 4 US-09-183-959-8 30 41 37.6 509 4 US-09-347-650-6 31 41 37.6 509 4 US-09-347-650-6 32 41 37.6 509 4 US-09-355-315-8 32 40 36.7 101 1 US-08-930-996A-8 35 40 36.7 357 3 US-09-188-579-79 35 40 36.7 357 3 US-09-188-579-79 36 40 36.7 357 3 US-09-1315-444-902 36 40 36.7 570 4 US-09-175-32A-4902 38 40 36.7 570 4 US-09-17-532A-4902 39 40 36.7 570 4 US-09-134-0000-5699 39 40 36.7 570 4 US-09-134-0000-5699 39 40 36.7 570 4 US-09-134-0000-5699 39 40 36.7 1058 2 US-08-484-438-10 40 36.7 1058 2 US-08-868-542C-35 44 39.5 36.7 1308 2 US-08-968-542C-35 44 39.5 36.7 1308 2 US-09-340-807-6 36.7 1308 2 US-09-340-807-6 36.7 1308 2 US-09-340-807-6 36.7 1308 2 US-09-340-807-6 36.7 1308 2 US-09-370-807-6 36.7 1308 2 US-09-370-8	ULI OULI EBAPE EBA	; SEQ ID NO 11 ; CLENGTH 19 ; TYPE: PRT ; CRGANISM: Dermatophagoides farinae US-09-292-225-11  Query Match Best Local Similarity 100.0%; Score 109; DB 4; Best Local Similarity 100.0%; Pred. No. 1.7e-11; Matches 19; Conservative 0; Mismatches 0; QY i DIPHPTNIHKYLVCESVNG 19 CM 1 DIPHPTNIHKYLVCESVNG 19 Db I DIPHPTNIHKYLVCESVNG 19 SESULT 2 US-09-292-225-3 ; Sequence 3, Application US/09292225 ; Patcht No. 6455666 ; GENERAL INFORMATION: APPLICANT: WCCall, Catherine A. APPLICANT: WCDer, Erick APPLICANT: WCDer, Shirley Wu APPLICANT: WCDer, Erick ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ; TITLE OF INVENTION: AND USES THEREOF

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CURRENT APPLICATION NUMBER: US/09/292,225
    TITLE OF INVENTION: AND USES THEREOF
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milarity 94.7%;
Conservative 0
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Best Local Similarity (
....hes 18; Conservat
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Best Local Similarity
Matches 18; Conserva
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US-09-292-225-41
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Sequence 21, Application US/0929225

Patent No. 645586

GENERAL INFORMATION:
APPLICANT: Mocall, Catherine A.
APPLICANT: Weber, Eric R.
ITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITLE OF INVENTION: AND USES THEREOF
ITLE OF INVENTION AND USES THEREOF
ITLE OF INVENTION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER PILING DATE: 1998-04-17
NUMBER: OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 536
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Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall. Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 19; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER APPLICATION NUMBER: 60/085,013
EARLIER PILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
LENGTH: 20

    TYPE: PRT
    ORGANISM: Dermatophagoides farinae
US-09-292-225-21

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; ORGANISM: Dermatophagoides farinae
US-09-292-225-3
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APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
APPLICANT: Hunter, Shirley Wu
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: USE THEREOF
FILE REPERBNCE: AL-2-3
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,295
BARLIER APPLICATION NUMBER: 60/085,295
BARLIER PATLING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTING DATE: 2.0
SEQ ID NO 18
LENGTH: 555
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0
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Pred. No. 6.6e-09;
0; Mismatches 1;
CURRENT FILING DATE: 1999-04-15
EARLIER PELICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER PILING DATE: 1998-09-02
EARLIER PILING DATE: 1998-05-13
EARLIER PILING DATE: 1998-04-17
EARLIER PELING DATE: 1998-04-17
EARLIER PILING DATE: 1998-04-17
EARLIER PILING DATE: 1998-04-17
EARLIER PILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN VET: 2.0
EARLIER PATENTIN VET: 2.0
EARLIER PILING DATE: 1998-04-17
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Patent No. 6455686
GENERAL INFORMATION:
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Sequence 18, Application US/09292225

Patent No. 6455686

GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-257-825B-21
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US-09-257-825B-20
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Sequence 35. Application US/0929225

Patent No. 645866

GarbraAL INFORMATION:

APPLICANT: Huncer, Shirley Wu
APPLICANT: Huncer, Shirley Wu
APPLICANT: Weber, Eric R.

ITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
ITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES,
ITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES,
ITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 1999-04-15

CURRENT FILING DATE: 1999-04-15

EARLIER APPLICATION NUMBER: 60/098,909

EARLIER FILING DATE: 1999-05-13

EARLIER FILING DATE: 1999-05-13

EARLIER FILING DATE: 1999-04-17

EARLIER FILING DATE: 1999-04-17

EARLIER FILING DATE: 1999-04-17

MANDED OF FILING DATE: 1999-04-17

MANDED OF FILING DATE: 1999-04-17
                     APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERNATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERNATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERNATOPHAGOIDES NUCLEIC ACID MOLECULES,
FILE REPERENCE: AL.2-C3
CURRENT APPLICATION NUMBER: US/09/292, 225
CURRENT APPLICATION NUMBER: US/098, 909
EARLIER APPLICATION NUMBER: 60/098, 909
EARLIER FILING DATE: 1998-09-12
EARLIER PILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 60/098, 565
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATECHIN VET. 2.0
SEQ ID NO 41
LENGTH: 490
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464 LPHPTDVHKYLVCEYIATPNG 484
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US-09-292-225-38
; Sequence 38, Application US/09292225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Dermatophagoides farinae US-09-292-225-41
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APPLICANT: Hunter, Shirley Wu
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 509
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NS-09-257-8258-21

Sequence 21, Application US/092578258

Patent No. 6403322

Jatent No. 6403223

CURRENT PILING DATE: 1999-02-25

PRIOR APPLICATION NUMBER: US/09/257,8258

PRIOR APPLICATION NUMBER: US/09/257,8258

PRIOR APPLICATION NUMBER: US/09/257,8258

PRIOR PILING DATE: 1996-02-25

PRIOR PILING DATE: 1996-03-28

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

JENGTH: 217
GENERAL INFORMATION:
APPLICANT: MCCall, Catherine A.
APPLICANT: HURCE.
APPLICANT: HURCE.
APPLICANT: HURCE.
APPLICANT: HURCE.
APPLICANT: HURCE.
APPLICANT: WCDEL, Exic R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TILE REFERENCE: AL-2-C3
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE PATENTING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 38
LENGTH: 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 517;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 4;
Pred. No. 0.51;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 20, Application US/09257825B; Patent No. 6403352; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 LPHPTDVHKYLVCEYIATPNG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Dermatophagoides farinae US-09-292-225-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IPHPTNIHKYLVCESV---NG 19
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Best Local Similarity 58.8%;
Matches 10; Conservative
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PATENT NO. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5038
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 23;
2; Mismatches 2; Indele
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                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE:
HILE OF INVENTION: FIBRINOLYTIC SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.5%; Pred. No. 17;
Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,413B
FILING DATE: October 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bothrops atrox moojeni
IMMEDIATE SOURCE:
CLONE: BATROXOBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|| ||: :: || |: |
135 DVPHCANINLFMNTVCREAYNG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5038, Application US/09328352
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-5038
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TELECOMULA.
TELEPAX: 212-753-623,
TELEPAX: 236687
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
"VDE: amino acids
"VDE: amino acids
"VDE: "WTS." include acids
"VDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
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                                    NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Darby & Darby
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: not
MOLECULE TYPE: I
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                     10022
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                                                           APPLICANT: Takezawa, Daisuke
TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
FILE REPERENCE: 4630-5199
CURRENT APPLICATION NUMBER: US/09/257,825B
CURRENT FILING DATE: 1999-02-25
PRIOR PILING DATE: 1996-05-23
PRIOR FILING DATE: 1996-05-23
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Version 3.1
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WS-08-933-711B-18

Sequence 18, Application US/08933711B

Sequence 18, Application US/08933711B

Sequence 18, Application US/08933711B

Sequence 18, Application

APPLICANT: Chuang, Pao-Tien

TILLE OF INVENTION: HEDGEHOG INTERACTING PROTEINS AND USES RELATED THERETO

FILE REFERENCE: HUV-024.01

CURRENT APPLICATION NUMBER: US/08/933,711B

CURRENT FILING DATE: 1997-09-19

PRIOR FILING DATE: 1996-09-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 18

LENGTH: 592
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US-08-933-711B-18
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Pred. No. 16;
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TITLE OF INVENTION: A NOVEL CDNA OF DIRECT-ACTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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Patent No. 5821106
GENERAL INFORMATION:
APPLICANT: CHUNG, Kwang-Hoe
APPLICANT: KCH, You-8eok
APPLICANT: HWANG, Jae-Hoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 VDHPDNINLTILCSDSNG 373
      APPLICANT: Poovaiah, Bachettira W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IPHPTNIHKYLVCESVNG 19
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38.9%;
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ORGANISM: Artificial Sequence
                                    Patil, Shameekumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Lilium longiflorum US-09-257-825B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIM, Doo-Sik
YUN, Yung-Dae
MOON, Hong-Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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APPLICANT:
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APPLICANT Network Control Application Application Application Network Application Network Application Network Application Network Application Network 
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STRAIN: ALKO4237
FEATURE:
                                                                                          RESULT 14
US-09-329-350-35
'Sequence 35, Application US/09329350
'Patent No. 6184019
                                                                                                                                                                                                                                                  Miettinen-Oinonen,
Londesborough, John
42 HPAKVHRYLV 51
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                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: RIESBECK, Kristian
APPLICANT: DORLING, Anthony
APPLICANT: GEORGE, Andrew
APPLICANT: LECHIER ROBERT
TITLE OF INVENTION: ANTICOAGULANT FUSION PROTEIN ANCHORED TO CELL MEMBRANE
FILE REFERENCE: 2222/0G135
CURRENT APPLICATION NUMBER: US/09/402,515A
CURRENT FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LIBRICH: 231
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                                                                                                 Length 452;
                                                                                                                                             6; Indels
                                                                                                 Score 43; DB 3;
Pred. No. 42;
3; Mismatches
; NAME/KEY: Protein
LOCATION: 1..452
; COCRTION: 1..452
; OTHER INFORMATION: /label= 50K-cellulase-B
US-09-329-350-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // TYPE: PRT
// ORGANISM: Agkistrodon contortrix contortrix
US-09-402-515A-16
                                                                                                 Query Match
39.4%; Score 43;
Best Local Similarity 43.8%; Pred. No. Matches 7; Conservative 3; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March 22, 2004, 07:03:57 Job time : 1.53141 secs
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US-09-402-515A-16
'Sequence 16, Application US/09402515A
'Patent No. 6423316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIPHPTNIH--KYLVCES 16
                                                                                                                                                                                                               249 PHACTINEYHVCETIN 264
                                                                                                                                                                                   3 PHPTNIHKYLVCESVN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.4
Matches 8; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 22, 2004, 06:40:28; Search time 1.30072 Seconds (without alignments) 1479.047 Million cell updates/sec Run on:

US-09-662-293-13 105 1 DPAKGMSPPGFIVGEEGVLS 20 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* PIR 78:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		hypothetical prote		๗	hypothetical prote		144	Ų		hypothetical prote		homeotic protein H	Ran-binding protei		hypothetical prote	hypothetical prote		hypothetical prote		related to trfA pr	hypothetical prote	alcohol dehydrogen	alcohol-acetaldehy	Clp ATPase [import	otei	hypX protein - Rhi	ble clp	Clp ATPase [import	햞	ATP-dependent Clp
		T13387	A86287	C87552	S09804	H72501	A99238	H72502	F70628	T02672	I55603	\$65775	S58884	F81444	AG2399	H70876	JC6087	E64028	AE3290	T51071	S53919	B95237	C98101	AE0358	544863	7261	$\mathbf{r}$	AH0437	2.	AD3090
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œ	Quer	. 4.	44.8	43.8	•	•	41.9	•	41.9	41.9	41.9	41.9	41.9	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	ä	ö	•	ö	•	•	٠
	Score	5		46	45	44	44	44	44	44	44	44	44	43	43	43	43	43	43	43	43	43	43	43		•	42.5			•
	ult No.		2	ო	4	Ŋ	9	7	α)	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote probable proteinas	collagen alpha 3(V hypothetical prote hypothetical prote	nypothetical prote late 100K protein sodium-glucose cot	probable ATPase SK leucine-tRNA synth inter-alpha-trypsi	aldehyde oxidase ( hypothetical prote hypothetical prote	Д
G90656 G85507	CGHU3A A87263 AE2164	H84378 WMAD40 A49112	149045 A84373 JC5576	A57429 AF2125 G87377	AD0314 AC3305
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923	3176 190 231	269 438 623	677 885 889	907	184
40.5	4. 4. 4. 0. 0. 0. 0. 0. 0.	0.04 0.00	4 4 0 . 0 0 . 0 0 .	9.04 0.04 0.04 0.04	39.0
2. 4. 4. 2. 2. 5.	4 2 4 4 5 2 2 5	4 4 4 9 6 6 6	4 4 4 0 0 0	41.5	4 4 1 1 1 1
30	6 6 6 6 5 6 4	33 34 34	ж с 4 8 Ф О	4 4 4 1 2 4 4	44 45

### ALIGNMENTS

RESULT 1

	hypothetical protein 115C2.8 - fruit fly (Drosophila melanogaster)	C;Species: Drosophila melanogaster	C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 19-Jan-2001	C, Accession: T13387	R,Salles, C.; Valenti, P.; Darlamitsou, A.; Henderson, N.; Campbell, L.; Glover,	submitted to the EMBL Data Library, May 1999	A, Description: Sequencing the distal X chromosome of Drosophila melanogaster.	A; Reference number: Z17665	A;Accession: T13387	A;Status: preliminary; translated from GB/EMBL/DDBJ	A; Molecule type: DNA	A; Residues: 1-408 <cat></cat>	A; Cross-references: EMBL: AL031581; NID: e1320978; PID: e1320993; PIDN: CAA20887.1	itics:	A;Cross-references: FlyBase:FBgn0020381	cons: 340/1	s: EG:115C2.8	C,Superfamily: Drosophila melanogaster hypothetical protein 115C2.8	cy Match 47.6%; Score 50; DB 2; Length 408;	18; Pred. No. 4.7;	thes 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
T13387	hypothetical	C; Species: Dr	C;Date: 13-Au	C; Accession:	R;Salles, C.;	submitted to	A; Description	A;Reference n	A; Accession:	A;Status: pre	A; Molecule ty	A; Residues: 1	A; Cross-refer	C,Genetics:	A; Cross-refer	A; Introns: 340/1	A; Note: EG:115C2.8	C; Superfamily	Query Match	Best Local	Matches

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# || :| || :::| : DPQEGFDPPTYLIGPDEELS 346 1 DPAKGMSPPGFIVGEEGVLS

à g

20

hypothetical protein F9L1.22 - Arabidopsis thaliana hypothetical protein F9L1.22 - Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiDate: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001
CiAccession: A66287
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Jin, X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Recession: A661817
A;Accession: A661877

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-573 <STO>

A; Cross-references: GB: AE005172; NID: 95103826; PIDN: AAD39656.1; GSPDB: GN00141

Score 47; DB 2; Pred. No. 21; 4; Mismatches

44.8%;

A; Map position: 1

C, Genetics:

Query Match

Best Local Similarity 47.1%; Matches 8; Conservative

| ||: ||: |:|| 477 PTFGMAYPGYVQSEDGV 493 2 PAKGMSPPGFIVGEEGV 18

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conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Dacession: AB9238
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Yoon, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. aubmitted to Genbank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein APE1998 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Aecies: Aeropyrum pernix
C;Accession: H75502
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kindh, Y.; Yamazaki, J.; Xin, Yamazaki, J.
hypothetical protein APE1990 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: H72501
A;Rawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jan-no, K.; Takahi A;Res. G. 33-101, 1999
A;Ritle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72501
A;Status: preliminary
A;Residues: 1-111 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;cross-references: DDBJ;AP000063; NID:g5105654; PIDN:BAA81000.1; PID:d1044786; PID:g5100
A;Experimental source: strain Kl
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A;Accession: A99238
A;Accession: A99238
A;Accession: A99238
A;Accession: Day
A;Molecule type: DNA
A;Residues: 1-408 «KUR»
A;Cross-references: GB:AE006641; NID:g13814052; PIDN:AAK41160.1; GSPDB:GN00155
C;Genetics: SGO872
C;Superfamily: hypothetical protein AF1590
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Pred. No. 9.6;
5; Mismatches 5; Indels
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C;Superfamily: Aeropyrum pernix hypothetical protein APE1990
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Pred. No. 42;
3; Mismatches
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85 EAARGVGPAGFPVFDDGV 102
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57.1%;
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 57.1
Matches 8; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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C;Species: human cytomegalovirus, human herpesvirus 5

A;Note: host Homo sapiens (man)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000

C;Accession: 509804

R;Chee, M. S.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;

M; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus A;Reference number: S09804

A;Acterns number: S09804

A;Accession: S09804

A;Accession: S09804

A;Accession: B09804

A;Accession: B09804

A;Crose-references: EMBL:XI7403; NID:G59591; PIDN:CAA35400.1; PID:e27240; PID:g1813967

A;Crose-references: EMBL:XI7403; NID:G59591; PIDN:CAA35400.1; PID:e27240; PID:g1813967

A;Note: this sequence was submitted to the EMBL Data Library, December 1989

A;Note: this reading frame extends between two stop codons and does not begin with a sta C;Superfamily: human cytomegalovirus hypothetical protein UL41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3

C89552

asparate transcarbamoylase, pyrC' subunit [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Accession: C87552

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salaberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. US.S. 98, 4136-4141, 2011

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: C87552

A;Status: preliminary

A;Residues: 1-433 <STO
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A;Gene: CC2444
C;Superfamily: Bacillus dihydroorotase; Bacillus dihydroorotase
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Pred. No. 8.7;
2; Mismatches 5; Indels
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Pred. No. 22;
4; Mismatches 9; Indels
                                                                                                              Length 573;
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DPESGYDGPGGVIVSEGVIT 35 1 DPAKGMSPPGFIVGEEGVLS 20

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43.8%; 40.0%;

Best\_Local Similarity 40.0 Matches 8; Conservative

Query Match

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/ Match 42.9%;
Local Similarity 53.3%;
les 8; Conservative
                                                                  AKDLPPPGYRVGRRG 90
                                            3 AKGMSPPGFIVGEEG 17
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Query Match

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CACCESSION: 155603
R;Yi, J. X. S.; Fernandez-Checa, J.; Kaplowitz, N.
J. Clin. Invest. 93, 1841-1845, 1994
A;Title: Expression cloning of a rat hepatic reduced glutathione transporter with canali A;Reference number: 155603; MUID:94216535; PMID:8163683
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A;Molecule type: mRT
A;Residues: 1-379, KS',381-1539 <WER>
A;Residues: 1-379,KS',381-1539 <WER>
A;Cross-references: EMBL:X89761; NID:g1143706; PIDN:CAA61910.1; PID:g1143707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Zea mays.
C;Species: Zea mays.
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2002
C;Accession: S65775; S72455
R;Kiinge, B.; Ueberlacker, B.; Korfhage, C.; Werr, W.
Plant Mol. Biol. 30, 439-453, 1996
A;Title: ZmHox: a novel 1class of maize homeobox genes.
A;Reference number: S65774; MUID:96189260; PMID:8605297
                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 07-Feb-1997
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     Gaps
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C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;802-858/Domain: homeobox homology <HOX1>
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     Indels
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A;Cross-references: EMBL:U06845; NID:g501037; PID:g501038
C;Keywords: liver
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53.8%; Pred. No. 1.9e+02;
live 3; Mismatches 3;
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Pred. No. 95;
     Mismatches
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64.3%;
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A, Cross-references: EMBL:X89761
                                                                                                              675 PAAGIPPPGLLTG 687
                                                        2 PAKGMSPPGFIVG 14
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Best Local Similarity 64.3
Matches 9; Conservative
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Best Local Similarity 53.88
Matches 7; Conservative
     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
     7;
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     Matches
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R;Color, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authores: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Nolecule type: DNA
A;Residues: 1-690 <COL>
A;Residues: 1-690 <COL>
A;Residues: 1-690 <COL>
A;Cossereferences: GB: Z84724; GB: AL123456; NID: 93261708; PIDN: CAB06578.1; PID: 91817674
A;Reperimental source: strain H37Rv
C;Genetics:
A;Gene: pta
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J.; Danganan, L.; Poundstone, P.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Ad
P.; Quan, G.; Kronmiller, B.; Arellano, A.; Montgomery, M.; Ow, D.; Nolan, M.
submitted to the EMBL Data Library, June 1998
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A;Description: Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a serine
A;Reference number: Z14696
A;Reference number: Z14696
A;Reference number: Z14696
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-813 < LAM>
A;Residues: 1-813 < LAM>
Cross-references: EMBL:AC005175; NID:g3253116; PID:g3253120
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A;Introns: 93/2; 125/2; 174/1; 228/2; 266/3; 331/1; 372/1; 474/3; 637/1; 678/3
A;Note: R31449_3
A,Residues: 1-410 <KAM>
A,Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA81008.1; PID:g5105696
A,Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                robable pta protein - Mycobacterium tuberculosis (strain H37RV)
;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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C;Species: Homo sapiens (man)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 31-Dec-2000
C;Accession: T02672
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                                                                                                                                                                                          Score 44; DB 2; Length 410;
Pred. No. 42;
3; Mismatches 4; Indels
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41.9%; Score 44; DB 2; Length 690;
Best Local Similarity 40.0%; Pred. No. 76;
Matches 8; Conservative 5; Mismatches 7; Indels
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92;
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Pred. No. 9
                         A.Cross-references: DDBJ.AP000063; NID:g510
A.Experimental source: strain Kl
C.Genetics:
A.Gene: APE1998
C.Superfamily: hypothetical protein AF1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 DALRRFTPPSYVVPEEPLLS 201
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53.8%;
                                                                                                                                                                                          Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                             47 QGSTPPSILVGERG 60
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Best Local Similarity
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330 DPVRGLDPLTAPGSIVEGARGLL
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30.8%;
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Best Local Similarity 47.8%;
Matches 11; Conservative
                                                                                                        120 POKGONPPKFHPGEK 134
              16
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Best Local Similarity
Matches 8, Conserva
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### SEARRA | Number | SEARRA |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Recular type: mRNA
A;Residues: 1-3224 <VOXA
A;Residues: 1-3224 <VOXA
A;Residues: 1-3224 <VOXA
A;Cross-references: EMBL:D42063; NID:g924266; PIDN:BAA07662.1; PID:g1009337
A;Cross-reference: cell type B-lymphocyte
B;Wu, J; Matunis, M.J; Kraemer, D; Blobel, G.; Coutavas, E.
A;Title: Nup358, a cytoplasmically exposed nucleoporin with peptide repeats, Ran-GTP bin
A;Reference number: A57545; MuID:95294031; PMID:7775481
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C;Species: Campylobacter jejuni
C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: F8144
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-669, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyparkerence number: A81250; MUDD:20150912; PMID:10688204
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C,Superfamily: nucleoporin Nup358, cyclophilin homology, tetratricopeptide repeat homold
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-291 <PAR>
A; Residues: 1-291 <PAR>
A; Cross-references: GB AL139074; GB: AL111168; NID: 96967505; PIDN: CAB72731.1; PID: 9696774
A; Experimental source: serotype O2, strain NCTC 11168
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A;Molecule type: mRNA
A;Residues: 1-776, "K',778-783, "R',785-3224 <WUA>
A;Residues: 1-776, "K',778-783, "R',785-3224 <WUA>
A;Cross-references: GB:L41840; NID:g857367; PIDN:AAC41758.1; PID:g657368
A;Experimental source: cell line HeLa
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47.4%; Pred. No. 4.4e+02;
iive 2; Mismatches 8; Indels
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F;60-31/Domain: tetratricopeptide repeat homology <TT2>
F;450-471/Domain: leucine zipper #status predicted <LEU>
F;3063-3224/Domain: cyclophilin homology <CYP>
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9; Conservative
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nes 8; Conservative
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A;Gene: GDB:RANBP2; NUP358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2cen-2q13
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Matches 9; Conserv
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C; Superfamily:
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Best Local S
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hypothetical protein all4751 [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
C,Species: Nostoc sp. PCC 7120
C,Species: Nostoc sp. PCC 7120
C,Species: Nostoc sp. strain PCC 7120
C,Date: Nostoc sp. strain PCC 7120
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C, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
NAkazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
NAccession: AG2399
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak
A,Accession: AG2399
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A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MJD: 98295987; PMID: 9634230
A; Reference number: A70500; MJD: 98295987; PMID: 9634230
A; Recession: H70876
A; Malequie rype: DNA
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A,Experimental source: strain H37Rv
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul_-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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52;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on: March 22, 2004, 06:31:13; Search time 0.767093 Seconds (without alignments)
1357.597 Million cell updates/sec
Title: US-09-662-293-13
Perfect score: 105
Sequence: 1 DPAKGMSPPGFIVGEEGVLS 20

Sequence: 1 DPAKGMSFPGFIVGEEGVLS 20 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Description	63 homo sap	P16814 human cytom	v	P19296 thermoprote	ä	P96254 mycobacteri			σ		P44184 haemophilus	C)		P34542 caenorhabdi		Q12608 emericella	_	Q9wtt2 rattus norv	_	P97280 mesocricetu	Q46509 desulfovibr		ralsto	gallu	oryza	P12330 oryza sativ		synechocy		P07019 escherichia	Q9h078 homo sapien	Q9z8a6 chlamydia p	m	
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## ALIGNMENTS

RESULT 1

Mol. Cell 4:563-571(1999).

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzatne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bonkfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Renertion and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM SHORT), AND VARIANT LEU-32.
MEDLINE=97390509; PubMed=9242611;
Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
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"Control of TRAIL-induced apoptosis by a family of signaling and decoy
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"Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";
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An antagonist decoy receptor and a death domain-containing receptor
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MEDLINE=97467318; PubMed=9325248;
MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
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MEDLINE-98090092; PubMed-9430227;
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.
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                                                                                              Science 277:815-818(1997).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       specificity in apoptotic initiation.";
Nat. Struct. Biol. 6:1048-1053(1999).
-!- FUNCTION: Receptor for He cytotoxic ligand TNFSF10/TRAIL. The adptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-
                                       Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I., Jones E.Y., Screaton G.R., "Structure of the TRAIL-DRS complex reveals mechanisms conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016021; C:integral to membrane; IC.
GO; GO:0016506; F:apoptosis activator activity; NAS.
GO; GO:0008656; F:caspase activator activity; NAS.
                    X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184
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AAR75587.1; -.
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EMBL; AF018657; AAB70577.1; -.
EMBL; AF016568; AAB71867.1; -.
EMBL; AF022386; AAB81180.1; -.
EMBL; AF022386; AAB671949.1; -.
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AB014716;
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AF020501;
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AB014710;
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EMBL;
EMBL;
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EMBL;
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us-09-662-293-13.rsp

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                 Gaps
                                                                                                                                                                                                                                                                            MEDLINE-90269039; PubMed=2161319; MEDLINE-90269039; PubMed=2161319; Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G. "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169."; Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1990 (Rel. 41, Last sequence update)
15-JUL-19910 (Hell 41, Last annotation update)
10. Inter-alpha-trypsin inhibitor heavy chain H3) (Inter-alpha-inhibitor heavy chain 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
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0
        Query Match
Best Local Similarity 43.8%; Pred. No. 7.8;
Matches 7; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.9%; Score 45; DB 1; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AA; 16766 MW; 20005377B1EFB712 CRC64;
                                                                                                                                                                                                                    Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Hypothetical protein UL41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        887 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X17403; CAA35400.1; -.
                                                        2 PAKGMSPPGFIVGEEG 17
                                                                              76 PSEGLCPPGHHISEDG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AKGMSPPGFIVGEEG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKDLPPPGYRVGRRG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S09804; S09804
Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blom A., Fries E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                       HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITH3 RAT
Q63416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                        UL41_HC
P16814
                                                                                                                RESULT 2
UL41_HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITIH3.
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Matches
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ITH3 RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                        SUBUNIT: 1-alpha-I plasma protease inhibitors are assembled from SUBUNIT: 1-alpha-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-alpha-L1) of H2 and bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin. PTM: Heavy chains are interlinked with bikunin via a chondroitin 4-sulfate bridge to the their C-terminal aspartate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINXED (GLCNAC. .) (POTENTIAL).
CHONDROITIN 4-SULFATE, CROSS-LINK SITE
(BY SIMILARITY).
3B9F0FF96D514096 CRC64;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTRIN BETWEEN HYALURONAN AND OTHER MATRIX PROTBIN, INCLUDING THOSE ON CELL SURPACES IN TISSUES TO REGULATE THE LOCALIZATION, SYMTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50234; VWFA; 1.
Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1989) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoproteus tenax virus 1 (strain KRA1) (TTV1).
Viruses; dsDNA viruses, no RNA stage; Lipothrixviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (strain KRA1) (TTV1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.9%; Score 45; DB 1; 47.1%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Hypothetical 26.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- Similarity: Belongs to the ITIH family.
-!- SimilaRity: Contains 1 WWPA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      887 AA; 99097 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X83231; CAA58233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR00587; VIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DPAKGMSPPGFIVGEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002035; VW
Pfam; PF00092; Vwa; 1.
SMART; SM00609; VIT; 1.
SMART; SMO0327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
33
647
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es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10480;
                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipothrixvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neumann H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
YORL_TTV1
ID YORL_TTV1
AC P19296;
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(See http://www.isb-sib.ch/announce/

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                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Olfactory epithelium;

XX SUBLENCE FROW N.A.

XX Tatabberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

A Straubberg R.L.; Feingold E.A.; Grouse L.H.; Schamen C.M.; Schuler G.D.;

X Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Diatchenko L., Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.,

Diatchenko L., Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.,

Brownstein M.J.; Uddin T.B.; Toshlyuki S., Carninci P.; Prange C.;

Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gubaratne P.H.;

Richarde S.; Worley K.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Richards S.; Worlby K.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Raha S.; Wurly D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Raha S.; World A., Schergen E.J.; Lu X.; Gibbs R.A.;

Raha S.; World A., Schergen E.J.; Lu X.; Gibbs R.A.;

Raha S.; World A.; Schengen E.D.; Dickson M.C.;

Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

Roberzation and initial analysis of more than 15,000 full-length

Rubman and mouse colk sequences.";

Rubman and manner descriptor and sequences.";

Rubman and mouse colk sequences.";

Rubman and manner descriptor and sequences.";
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rowen L., Qin S., Madan A., Loretz C., Hall J., James R., Dors M., Shaffer T., Abbasi N., Ratcliffe A., Dickhoff R., Lasky S., Hood L.; "Sequence of the mouse major histocompatibility complex class II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                     Score 44; DB 1; Length 232;
Pred. No. 16;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 ll protein.
232 AA; 26862 MW; 0ABC274AF657CA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. Ü.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FRAR-2004 (Rel. 43, Last annotation update)
WD_repeat protein BING4.
                                                                                                                                                                                                       EMBL; X14855; CAA32992.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                          41.9%;
54.5%;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                           176 PPGQLIGDEGI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              8 PPGFIVGEEGV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=129/SvJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIN4 MOUSE
Q9Z0H1;
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
BIN4_MOUSE
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MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
Gordon S.V., Encoch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Genles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLenn J., Molloy M., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sniston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAINECDC 1551 / Oshkosh;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
Meterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Rollonay J.F., Nelson W.C., Umayam L.A., Ernouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Wenter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phosphate acetyltransferase (EC 2.3.1.8) (Phosphotransacetylase).
PTA OR RV0408 OR MT041 OR MTCY22G10.04.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphate. -!- PATHWAY: Conversion of acetate to acetyl-CoA; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                             41.9%; Score 44; DB 1; Length 622; 77.8%; Pred. No. 46; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                B1BF9A36AC612612 CRC64;
                                          EMBL; AF110520; AAC97976.1; -.
EMBL; AF100956; AAC69896.1; -.
EMBL; BC046977; AAH46977.1; -.
EMBL; BC046977; BING4.
INCEPTO; IPRO01680; WD40.
Pfam; PPO0400; WD40; 1.
SMART; SM00320; WD40; 3.
PROSITE; PS00678; WD REPEATS_1; FALSE_NEG.
PROSITE; PS00678; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690 AA.
entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                69048 MW;
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Matches 7; Conservative
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156 PGFLVGEDG 164
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622 AA;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: IN THE N-TERMINAL SECTION; CONTAINS A DOMAIN WITH SOME SIMILARITIES WITH COBQ/BIOD.
SIMILARITY: In the C-terminal section; belongs to the phosphate acetyltransferase and butyryltransferase family.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.96 ANGSTROMS) OF 1171-1304.
MEDLINE=99176415; PubMed=10078529;
Vetter I.R., Nowak C., Nishimoto T., Kuhlmann J., Wittinghofer A.;
"Structure of a Ran-binding domain complexed with Ran bound to a GTP analogue: implications for nuclear transport.";
Nature 398:39-46(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=95294031; PubMed=7775481;
Wu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E.;
"Nup358, a cytoplasmically exposed nucleoporin with peptide repeats,
"Ran-GTP binding sites, zinc fingers, a cyclophilin A homologous
domain, and a leucine-rich region.";
J. Biol. Chem. 270:14209-14213(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P49792; Q15280;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ran-binding protein 2 (RanBP2) (Nuclear pore complex protein Nup358)
(Nucleoporin Nup358) (358 kDa nucleoporin) (P270).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yokoyama N., Hayashi N., Seki T., Nishii K., Hayashida T., Kuma K.I., Miyata T., Fukui M., Nishimoto T., Pante N., Aebi U., "A giant nucleopore protein that binds Ran/TC4."; Nature 376:184-188(1995).
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                                                                                                                                                                                                                  TLOK; M. 1972...
TLOK; M. 1972...
TLOK PARTIES P. 1974...
INTERPOS I PR002505; PTA PTB.
Elam, PP01515; PTA PTB. 1.
TIGREMAS; TIGROSO651; PTA; 1.
TIGREMAS; TIGROSO651; PTA; 1.
TIGREMAS; TIGROSO651; PTA; 1.
TIGREMAS TIGROSO651; PTA; 1.
TIGREMAS TIGROSO651; PTA; 1.
TRANSFERSE, ACYLLANSFERSES.
SEQUENCE 690 AA; 72948 MW; COIC412AF2810CCE CRC64;
                                                                                                                                                                                                                                                                                                                                  41.9%; Score 44; DB 1; Length 690;
40.0%; Pred. No. 52;
tive 5; Mismatches 7; Indels
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                                                                                                                                                                                    EMBL; AE006946; AAK44645.1; -. PIR; F70628.
TIGR; MT0421; -.
                                                                                                                                                                          EMBL; Z84724; CAB06578.1; -.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.00,
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MIMM, 601181; --

RO, GO:0005643; C:nuclear pore; TAS.

RO, GO:0005643; C:nuclear pore; TAS.

RO, GO:0005605; P:Protein binding; TAS.

RO, GO:0006506; P:Protein-nucleus import; TAS.

RICEPPO; IPR000130; CSA_PPIASe.

RICEPPO; IPR000150; EWHI.

RICEPPO; IPR000150; EWHI.

RICEPPO; IPR00140; TPR-like.

RICEPPO; IPR00140; TPR-like.

RICEPPO; IPR00140; TPR-like.

RICEPPO; IPR00150; RANGDP.

RICEPPO; IPR00150; RANGDP.

RICEPPO; IPR00151; APR-like.

RICEPPO; IPR00151; APR-like.

RICEPPO; RANGDP.

RICEPPO; IPR00151; APR-like.

RICEPPO; IPR00151; APR-like.

REAM; PR00151; APR-like.

REAM; PR00151; APR-like.

REAM; RR00151; CSAPPISMRASE.

REAM; SMO0160; RANBD; 4.

RROSITE; PS00170; CSA_PPIASE 1; 1.

RROSITE; PS00129; ZF_RANBP2 1; 8.

RROSITE; PS01359; ZF_RANBP2 1; 8.

RROSITE; PS01359; ZF_RANBP2 2; 1.

RROSITE; PS01359; ZF_RANBP2 2; 8.

UNCTION: Involved in transport factor (Ran-GTP, karyopherin)-
mediated protein import via the F-G repeat-containing domain which
acts as a docking site for substrates. Could also have isomerase
or chaperone activity and may bind RNA or DNA. Component of the
nuclear export pathway. Specific docking site for the nuclear
export factor exportin-1.
SUBUNIT: Forms a tight complex in association with RANBPI and the
                                                                                                                                                                                                                                                                                                                ubiquitin-conjugating enzyme E2 (UBC9) (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear pore complex. Cytoplasmic filaments.
-!- DOMAIN: Contains F-X-F-G repeats.
-!- SIMILARITY: Contains 4 RanBDI domains.
-!- SIMILARITY: Contains 8 RANBP2-type zinc fingers.
-!- SIMILARITY: Contains 1 cyclophilin-like PPlase domain.
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PPIASE CYCLOPHILIN-TYPE.
P -> A (in dbSNP:12770).
/FITG=VAR 014886.
R -> H (IN REF. 2).
R -> K (IN REF. 2).
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EMBL; D42063; BAA07662.1; -.
PIR; S58884.
PBB; IRRF; 18-MAY-99.
Genew; HGNC:9848; RANBP2.
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Gaps

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Indels

41.0%; Score 43; DB 1; 53.3%; Pred. No. 29;

2; Mismatches

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291 AA; 31462 MW; 35A0E51E408E1CF2 CRC64;
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  SEQUENCE
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BET3_MESAU
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Matches
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SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: Belongs to the ZIP transporter (TC 2.A.5) family. ZupT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=20150912; PubMed=10688204; Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Fellwell T., Holroyd S., Quall M.A., Ralyshev A.V., Moule S., Pallen M.J., Penn C.W., Quall M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; Whitehead S., Barrell B.G.; Whitehead S., Barrell B.G.; Natherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; Pallen pathogen Campylobacter jejuni reveals hypervariable sequences."; Nature 403:665-668(2000).
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBL_TaxID=197;
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                                                                                                                                                                                                                    Score 44; DB 1; Length 3224;
Pred. No. 2.7e+02;
2; Mismatches 8; Indels
                  1255 1255
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1301 1302
3224 AA; 358214 MW; 54E78412C96A3C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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InterPro; IPR003689; Zn_transpt_Zip.
Pfam; PF02535; Zip; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                           2505 PKAVVSPPKFVFGSESVKS 2523
                                                                                                                                                                                                                                                                                                    2 PAKGMSPPGFIVGEEGVLS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL139074; CAB72731.1; -. PIR; F81444; F81444.
                                                                                                                                                                                                             Query Match
Best Local Similarity 47.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc transporter zupT. ZUPT OR CJ0263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NCTC 11168;
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Q9PIN2;
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AUD _ZUPT_CAMJE

DT _28-FEB

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H
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Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kashida Y., Kohara M., Matsumoto M., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

Complete genomic sequence of the filamentous nitrogen-fixing

Tyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).

IDNA Res. 8:205-213(2001).

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                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable inorganic polyphosphate/ATP-NAD Kinase 1 (EC 2.7.1.23)
(Poly(P)/ATP NAD kinase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 PIDGLTPPGFDSEMKFAIVLGGDGTV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP003597; BAB76450.1; -. PIR; AG2399; AG2399.
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009029;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anabaena sp. (strain PCC 7120)
                                                120 POKGONPPKFHPGEK 134
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Best Local Similarity 30.00,
2 PAKGMSPPGFIVGEE 16
                                                                                                                                                                                                                                                                                                                             STANDARD;
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EMBL; U32820; AAC23058.1; -. PIR; E64028; E64028.
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                                                                                                                                     Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 394 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                 TIGR; HI1410;
                                                                                                           Venter J.C.;
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059942;
                                                                                                                                                                                                                                                                                                                                                                                                                                              186
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AAP2_NEUCR
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                                                                                                                Gaps
                                                                              SEQUENCE FROM N.A.
MEDLINE-96140430; PubMed-8552091;
Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.0%; Score 43; DB 1; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6CAB9AFF96E85F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       regulation; Repressor
                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLY.
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YE10 HAEIN STANDARD; PRT; 394 AA. P44184; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) Protein H11410.
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 38;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               POLY-ALA.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLY.
POLY-GLY.
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                  BETA3 protein.
Mesocricetus auratus (Golden hamster)
                                                                                                                                                                                                                                                                                                                      TRANSFAC; T01674; -...
InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
PRART; SM00353; HLH; 1.
PROSITE; PS50898; HLH; 1.
Nuclear protein; Transcription re
                                                                                                                                                                                                                                                                                                                                                                                                                                                       35905 MW;
                                                                                                                                                                                                                                                                                                                EMBL; S80870; AAB50691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GMSPPGFIVGEEGV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
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174
204
229
241
311
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=727;
                                                     Mesocricetus
                                                                                                           Tsai M. -J.;
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DOMAIN
DOMAIN
DNA BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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YE10 HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome random sequencing and assembly of Haemophilus influenzae
MEDLINE=95350630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Felischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedlom E. Cotton M.D., Pine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B., Gray C., Fountoulakis M., "Two-dimensional map of the proteome of Haemophilus influenzae."; Electrophoresis 21:411-429(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MARGOLIGE-Clark E., Bowman B.J.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the amino acid permease family.
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Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Amino acid permease 2.
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1; Mismatches
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InterPro; IPR006437; Phage_term_2.
Pfam; PF04466; G2P; 1.
TIGRFAMS; TIGR01547; phage_term_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
IDENTIFICATION BY MASS SPECTROMETRY.
MEDLINE=20137488; PubMed=10675023.
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Gaps

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Indels

Length 817;

Score 43; DB 1; Pred. No. 89;

41.0%; ilarity 36.8%; Conservative

4; Mismatches

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PIR, S53919, S53919.

GermOnline; 141508; -.

SGD, S0003428; FYV8.

GQD; GO:0005737; C:Cytoplasm; IDA.

Hypothetical protein.

SEQUENCE 817 AA; 90797 MW; E52C5D659D63BEBB CRC64;
                                                                                                                                                                                                                                                   1 DPAKGMSPPGFIVGEEGVL 19
                                                                                                                                                                             Local Similarity
nes 7; Conserv
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                                                                                                                                                                 Query Match
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         % ₹₽₽₽₽
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete sequence of a 9000 bp fragment of the right arm of Saccharomyces cerevisiae chromosome VII contains four previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last amortation update)
47pothetical 90.8 kDa protein in RRP41-SNG1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guerreiro P., Maia e Silva A., Barreiros T., Arroyo J.,
Garcia-Gonzalez M., Garcia-Saez M.I., Rodrigues-Pousada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 1; Length 551;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C812C646B82F9ADF CRC64;
                                                                                                                             EMBL; AF053231; AAC08355.1; -.
InterPro; IPR002293; AA/rel permeasel.
InterPro; IPR004756; AA_permease.
InterPro; IPR004841; Permease region.
FinerPro; IPR004841; Permease region.
InterPro; IPR004841; Permease region.
InterPro; IPR00907; 2A0304; 1.
ITGRFAMS; TIGR00907; 2A0304; 1.
ITANSPORTE; PAMINO_ACID ACID PERMEASE 1; 1.
ITANSPORT; AMINO_ACID ACID ERMEASE 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
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Yeast 11:1087-1091(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59869 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.0%;
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YG4A_YEAST
ID YG4A_YEAST
AC P46949;
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TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craston M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Latrefile P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownken R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan R.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
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Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                 P34542; P34543;
01-FBB-1994 (Rel. 28, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Hypothetical protein R05D3.9 in chromosome III precursor.
R05D3.9/R05D3.10
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58.8%; Pred. No. 82;
live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE=94150718; PubMed=7906398;
547 DTANKKAPPGYVIDSNGKL 565
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PIR; S44865; S44865.
WormPep; R05D3.9; CE31049.
Hypothetical protein; Signal.
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                                                                                                                                                                           STANDARD;
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Best Local Similarity
Lac 10; Conserva
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MEDLINE=95182468; PubMed=7533217;
Arnoux B., Merigeau K., Saludjian P., Norris F., Norris K., Bjoern S., Olsen O., Petersen L., Ducruix A.;
"The 1.6 A structure of Kunitz-type domain from the alpha 3 chain of human type VI collagen.";
J. Mol. Biol. 246:609-617(1995). SECUENCE OF 2092-2157 FROM N.A.
MEDLINE-88029444; PubMed=3665927;
Chu M.-L., Mann K., Deutzmann R., Pribula-Conway D.,
Hsu-Chen C.-C., Bernard M.P., Timpl R.;
"Characterization of three constituent chains of collagen type VI by peptide sequences and cDNA clones.";
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TISSUB-Fibroblast;
MEDLINE-90151612; bubMed=1689238;
MEDLINE-90151612; bubMed=1689238;
GLU M.-L., Zhang R.-Z., Pan T.-C., Stokes D., Conway D., Kuo H.-J.,
Glanville R., Mayer U., Mann K., Deutzmann R., Timpl R.;
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alpha 3 chain: similarity to von Willebrand factor, fibronectin,
actin, salivary proteins and aprotinin type protease inhibitors.";
EMBO J. 9:385-393(1990). SEQUENCE OF 2038-2373 FROM N.A.
MEDLINE=8906644; PubMed=3198591;
Chu M.-L., Conway D., Pan T.-C., Baldwin C., Mann K., Deutzmann R., Timpl R.;
"Amino acid sequence of the triple-helical domain of human collagen type VI.";
J. Biol. Chem. 263:18601-18606(1988). SEQUENCE OF 2092-2151 FROM N.A.
TISSUB=Placenta;
TISSUB=Placenta;
TISSUB=Placenta;
TISSUB=Placenta;
TISSUB=Placenta;
TISSUB=Placenta;
Weil D., Mattel M.-G., Passage E., van Cong N., Pribula-Conway D., Weil D., Mattel M.-G., Timpl R., Chu M.-L.,
"Cloning and chromosomal localization of human genes encoding the three chains of type VI collagen.",
Am. J. Hum. Genet. 42:435-445(1988). SECUENCE OF 32-236 FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=93054780; PubMed=1339440;
Zanussi S., Doliana R., Segat D., Bonaldo P., Colombatti A.;
The human type VI collagen gene. mRNA and protein variants of the alpha 3 chain generated by alternative splicing of an additional 5. exon."; Euteleostomi; Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo Chu M.-L.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases. X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 3107-3164 CA36 HUMAN STANDARD; PRT; 3176 AA. P12111; 016501; 01-0CT-1989 (Rel. 12, Created) 10-UTL-1999 (Rel. 38, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Collagen alpha 3(VI) chain precursor. Biol. Chem. 267:24082-24089(1992). 17 28 PAKGMSPPG-FIVGEEG 42 PPSGPSPPGKFPDGDEG Homo sapiens (Human) NCBI\_TaxID=9606; REVISIONS COLGA3 RESULT 15 CA36\_HUMAN DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDT g à

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Isold=P12111-2; Sequence=VSP 001172;

-I- FTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.

-I- DISEAGE: Defects in COL6A3 are a cause of Bethlem myopathy (BM) [MIM:158810]. BM is a rare autosomal dominant proximal myopathy characterized by early childhood onset (complete penetrance by the age of 5) and joint contractures most frequently affecting the elbows and ankles.

-I- DISEASE: Defects in COL6A3 are a cause of Ullrich congenital muscular dystrophy (UCMD) [MIM:254090]; also known as Ullrich scleroatonic muscular dystrophy. UCMD is an autosomal recessive congenital myopathy characterized by muscle weakness and multiple joint contractures, generally noted at birth or early infancy. The clinical course is more severe than in Bethlem myopathy.

-I- SIMILARITY: Contains I BPTI/Kunitz inhibitor domain.

-I- SIMILARITY: Contains 12 VWFA domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myopathy.";
Hum. Mol. Genet. 7:807-812(1998).
-!- FUNCTION: Collagen VI acts as a cell-binding protein.
-!- SUBUNIT. Trimers composed of three different chains: alpha 1(VI),
alpha 2(VI), and alpha 3(VI).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                  "Structure and multiple conformations of the Kunitz-type domain from human type VI collagen alpha3(VI) chain in solution."; Structure 4:195-209(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Solution structure and backbone dynamics of the human alpha3-chain type VI collagen C-terminal Kunitz domain."; Biochemistry 36:10439-10450(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21987636; PubMed=11992252; Demir E., Sabatelli P., Allamand V., Ferreiro A., Moghadaszadeh B., Makrelouf M., Topaloglu H., Echemne B., Merlini L., Guicheney P.; Mutations in COL663 cause evere and mild phenotypes of Ullrich congenital muscular dystrophy."; Am. J. Hum. Genet. 70:1446-1458 (2002).
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MEDLINE=98204804; PubMed=9536084;

Pan T.-C., Zhang R.-Z., Pericak-Vance M.A., Tandan R., Fries T.,
Stajich J.M., Viles K., Vance J.M., Chu M.-L., Speer M.C.;

"Missense mutation in a von Willebrand factor type A domain of the alpha 3(VI) collagen gene (COL6A3) in a family with Bethlem
                                STRUCTURE BY NMR OF 3102-3164.
MEDLINE-96398604; PubMed-8805527;
Zweckstetter M., Czisch M., Mayer U., Chu M.-L., Zinth W., Timpl
                                                                                                                                                                                                                                                                                                                                       MEDLINE-97410331; PubMed=9265624; Soerensen M.D., Bjoern S., Norris K., Olsen O., Petersen L., James T.L., Led J.J.;
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IsoId=P12111-1; Sequence=Displayed;
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EMBL, X06196, CAA29557.1; -.
EMBL, M20778; -; NOT ANNOTATED_CD EMBL, M27449; AA52057.1; -.
EMBL, S4942; AAB24261.1; -.
PIR, A59140; CGHU3A.
                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 3107-3164
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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BPTI/KUNITZ INHIBITOR.
CELL ATTACHMENT SITE.
                                                                                                                                         VWFA 1.
VWFA 3.
VWFA 4.
VWFA 5.
VWFA 5.
VWFA 7.
VWFA 10.
VWFA 10.
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Best Local Similarity
Matches 8; Conservat
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Gaps

Search completed: March 22, 2004, 06:53:02 Job time : 0.767093 secs

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March 22, 2004, 06:39:53 ; Search time 4.02446 Seconds (without alignments) 1568.003 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                 1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
                                                                                                                                                             US-09-662-293-13
105
1 DPAKGMSPPGFIVGEEGVLS 20
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sp_human:*
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sp_mammal:*
sp_mammal:*
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sp_blant:*
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sp_vlrus:*
sp_vertebrate:*
                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                 Minimum DB seg length: 0
Maximum DB seg length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL
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Perfect score:
                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                  Searched:
                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp archeap:\*

	Description	r7	Q8mrz9 drosophila	Q9w5e2 drosophila	Q7z360 homo sapien	Q82sj2 nitrosomona	Q9xi41 arabidopsis		Q8h1f3 arabidopsis		Q8e2d5 streptococc	Q7x4k8 synechococc	Q8rjy9 stigmatella	Q9a5k3 caulobacter	Q8h849 oryza sativ	Q974c3 sulfolobus	Q8aw10 brachydanio
SUMMARIES	CI	Q9U6R7	Q8MRZ9	Q9W5E2	072360	Q82SJ2	Q9XI41	QBRXP2	Q8H1F3	QBE7U2	QBB2D5	Q7X4K8	QBRJY9	Q9A5K3	Q8H849	Q974C3	Q8AW10
	80	'n	S	Ŋ	4	16	10	10	10	16	16	7	7	16	10	17	13
	Query Match Length DB	555	408	408	118	201	573	584	585	880	880	198	144	433	455	662	3075
οķο	Query	94.3	47.6	47.6	45.7	44.8	44.8	44.8	44.8	44.8	44.8	44.3	43.8	43.8	43.8	43.8	43.8
	Score	66	50	20	48	47	47	47	47	47	47	46.5	46	46	46	46	46
	Result No.	н	(1)	m	4	ഗ	9	7	00	თ	10	11	12	13	14	15	16

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Query Match

94.3%; Score 99; DB 5; Length 555;
Best Local Similarity 95.0%; Pred. No. 3.7e-07;
Matches 19; Conservative 0; Mismatches 1; Indels

O75592 homo sapien Q7tph6 mus musculu Q98jt1 rhizobium 1 039919 human cyrom Q8a3y9 bacteroides Q8a1p1 bacteroides Q8mmd1 corynebacte Q8pp13 xanthomonas Q8mz10 drosophila Q91z98 mus musculu Q8y443 mus musculu Q8y443 mus musculu Q8y444 with column Q8y74 vibrio vuln Q8y74 vibrio vuln Q8y77 vibrio vuln Q8y20 cryptospori Q8y20 methanosarc Q90z65 cryptospori Q8y20 methanosarc Q90z65 tribolium c Q8730 neurospora Q8730 neurospora Q8730 neurospora Q8730 neurospora Q8720 sulfolobus Q8720 sulfolobus Q9yael aeropyrum p Q8720 sulfolobus Q9yael aeropyrum p	PRIGNMENTS  1 UGR7  1 Q9UGR7  1 Q9UGR7  2 GRG 7 PRELIMINARY; PRT; 555 AA.  2 G9UGR7  2 GRG 7 GTEXBLrel. 13, Created)  1 Last sequence update)  2 Last annotation update)  3 Last sequence update)  3 Last sequence update)  3 Last sequence update)  4 Last annotation update)  5 Last annotation update)  5 Last annotation update)  6 Last annotation update)  6 Last annotation update)  6 Last annotation update)  7 Last alergen.  8 Expra HDM alergen.  8 Expra HDM alergen.  8 Expraylphidae, Dermatophagoides.  8 Exprodivence; Sarcoptiformes; Astigmata, Psoroptidia; Analgoidea;  8 Progivence FROM N.A.  8 Expuser FROM N.A.  8 Expuser FROM N.A.  8 SEQUENCE FROM N.A.  8 SEQUENCE FROM N.A.  8 SEQUENCE FROM N.A.  9 RATE (101)  9 Submitted (102-199)  10 the EMBL/GenBank/DDBJ databases.  11 Submitted (102-199)  12 GO:0005576; Createdlular; IEA.  13 GO:0005576; Createdlular; IEA.  14 GO: GO:000577; Prodicin binding; IEA.  15 GO: GO:000577; Prodicin metabolism; IEA.  16 GO: GO:000577; Prodicin metabolism; IEA.  17 GO: GO:0006017; Prodicin metabolism; IEA.  18 FROM PRODOS77; Chitin bind PerA.  19 FRODON; PRODIS79; Glyco_Hydro_18; 1.  10 SMART; SWO0494; ChEDD? 1.  11 SMART; SWO0494; ChEDD? 1.  12 FROM PRODOS7; Glyco_Hydro_18; 1.  13 FROM PRODOS7; Glyco_Hydro_18; 1.  14 FROM PRODOS7; Glyco_Hydro_18; 1.  15 FROM PRODOS7; Glyco_Hydro_18; 1.  16 SWART; SWO0494; ChEDD? 1.  17 FROM PRODON; PRODOS7; Glyco_Hydro_18; 1.  18 FROSITER; PSO1095; GliffinAsE_18; 1.  18 FROSITER; PSO1095; GliffinAsE_18; 1.
	ALIGNMENTS  RT; 555 P  ated) t sequence t annotatic -dust mite) Chelicerat tigmata; Ps  K., McCall f a 98 kDa L/GenBank/D  i IEA. ivity, acti metabolism; metabolism; liem; IEA. ivity, acti liem; IEA. ivity, acti metabolism; liem; IEA. ivity, acti
075592 077PH6 098JT1 088J2Y 08AJ2Y 08NWD1 08PBL3 080J2A 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J2 080J	ALIGNMENTS  THRY; PRT; 555 AA.  Tel. 13, Created) Tel. 13, Last sequence updather.  Tel. 25, Last annotation updather.  Arthropoda; Chelicerata; Ar.  Tiformes; Astigmata; Psoropticomes; Astigmata; Psoropticomes; Astigmata; Psoropticophagoides.  To the EMBL/GenBank/DDBU duerication of a 98 kDa Aller; to the EMBL/GenBank/DDBU duerication of a 98 kDa Aller; tracellular; IEA.  The Cohe EMBL/GenBank/DDBU duericate metabolism; IEA.  Titracellular; IEA.  Glyco-hydro-18.  Glyco-hydro-18.  Glyco-hydro-18; 1.  Tyco-hydro-18; 1.  Tyco-hydro-18; 1.  Tyco-hydro-18; 1.  TiTINASE-18; 1.  TITINASE-18; 1.
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	PRELIMINARY; (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 13, Idea farinae (Ho fetazoa; Arthropo fetazoa; Anthropo fetazoa; Antrop fetazoa; Anthropo fetazoa; A
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SEQUENCE FROM N.A.
STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
MEDLINE=22586410; PubMed=12700255;
Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.,
"Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautcortoph Nitrosomonas europaea.";
J. Bacteriol. 185:2759-2773 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Human colon endothel primary cell culture;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
Hypothetical protein.
SEQUENCE 118 AA; 12808 MW; 0310EF97EIF0E92C CRC64;
                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nitrosomonas europaea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 48; DB 4; Length 118; 43.8%; Pred. No. 9; cive 5; Mismatches 4; Indels
 Length 408
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                                       Indels
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Pfan, PP03872; RseA_N: 1.
Hypchetical protein; Complete proteome.
Hypchenc 201 AA; 22079 MW; C5364D2B5BCD1A45 CRC64;
                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
Score 50; DB 5;
Pred. No. 16;
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 47.6%; Score 50; DB llarity 40.0%; Pred. No. 16; Conservative 5; Mismatches
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01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
Hypothetical protein DKFZp686I01145.
DKFZP686I01145.
                                                                                                                 327 DPQEGPDPPTYLIGPDEELS 346
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NCBI_TaxID=915;
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                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
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Query Match
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Matches 8; Conserv
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01-0CT-2003
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Q82SJ2;
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Flybase; Fagn0025634; EG:115C2.8.
SEQUENCE 408 AA, 43953 MW; 0FDS1AE3C6303960 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Salles C., Valenti P., Darlamitsou A., Henderson N., Campbell L.,
Glover D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequencing the distal X chromosome of Drosophila melanogaster.", submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                            EG:115C2:8 OR CG13367.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Bukaryota, Endopterygota, Diptera; Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
47.6%; Score 50; DB 5; Length 408;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 8; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
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EMBL; AL031581; CAA20887.1; -...
PIN; T13387; T13387.
FLYBase; FEGD0025634; EG:115C2.8.
SEQUENCE 408 AA; 43939 NW; 8B9E0E52E0886F4F CRC64;
                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                          298 DPAKGMSPPGFISGEEGVLS 317
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                       DPAKGMSPPGFIVGEEGVLS
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SEQUENCE FROM N.A.
STRAIN=NEM316 / Serctype III;
MEDLINE=2224508; PubMed=12354221;
Glaeer P., Rueniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neomatal disease.";
Invasive neomatal disease.";
Microbiol. 45:1459-1513 (2002).
EMBL, AL766843, CA045698.1; -..
SagaList; Gb80053; -..
SagaList; Gb80053; -..
GO; GO:0005506; F:irron ion binding; IEA.
GO; GO:0016491; F:cardoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.8%; Score 47; DB 10; Length 585; 47.1%; Pred. No. 73; 1ve 4; Mismatches 5; Indels
DB 10; Length 584;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECKET J.R., Theologis A.;
"Arabidopsis Open Reading Frame (ORF) Clones.";
Submitted (SEP: 2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY150428; AAN12370.1;
Hypothetical protein.
SEQUENCE 585 AA; 63435 MW; SEOFF3FBDD185A15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                        ıņ
                                                                                                                                                                                                                              585 AA.
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                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                       ATIG15280.
Arabidopsis thaliana (Mouse-ear cress).
Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                      | ||: ||:: |:||
478 PTFGMAYPGYVQSEDGV 494
                                                                                   2 PAKGMSPPGFIVGEEGV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PAKGMSPPGFIVGEEGV 18
44.8%;
47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 47.1 ses 8; Conservative
                   Best Local Similarity 47.1 Matches 8; Conservative
                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
  Query Match
                                                                                                                                                                                                                              Q8H1F3
Q8H1F3;
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Q8E7U2;
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Goldemith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. Columbia;

STRAIN-CV. columbia;

Vysoteskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
Altafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L.,
Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C.,
Federspiel N.A., Theologis A.;
Federspiel N.A., Theologis A.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007591; AA0139656.1;
PERE, AA6287; A86287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
ATIG15280.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; errosids il; Brassicales; brassicaceae, Arabidopsis.
NUBL TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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"Arabidopsis Full Length cDNA Clones.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY08076-1 protein.
Hypochetical protein.
SEQUENCE 584 AA; 63284 MW; 5DD94B2B05B83B43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573 AA; 62034 MW; CD6F93983F1ADC84 CRC64;
                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                  573 AA
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F9L1.22.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                          Created)
                                                                                                                                                                PRT;
                                        181 PATGISSPAEVVGEOSAAS 199
                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 PTFGMAYPGYVQSEDGV 493
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                   PAKGMSPPGFIVGEEGVLS
                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 47.17
Best Local 8; Conservative
                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
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QBRXP2; QBRXP2

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Matches

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PubMed=12775703;
Perelman A., Uzan A., Hacohen D., Schwarz R.;
"Oxidative Stress in Synechococcus sp. Strain PCC 7942: Various
Mechanisms for H(2)O(2) Detoxification with Different Physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The biosynthesis of the aromatic myxobacterial electron transport inhibitor stignatellin is directed by a novel type of modular polyketide synthase."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ421825; CAD19082.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sg al5;
Gaitatzis N., Silakowski B., Kunze B., Nordsiek G., Blocker H.,
Hofle G., Muller R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacieria, Proteobacteria, Deltaproteobacteria, Myxococcales,
Cystobacterineae, Cystobacteraceae, Stigmatella.
NCBI_TaxID=41;
                                                                                                                                                                     Symechococcus sp. (strain PCC 7942) (Amacystis nidulans R2).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

84.3%; Score 46.5; DB 2; Length 198;
Best Local Similarity 50.0%; Pred. No. 27;

Matches 10; Conservative 6; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15573 MW; 0283C9FF87BF8B55 CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosome binding factor.
               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 185:3654-3660(2003).
EMBL; AF492495; AAP49028.1; -.
Peroxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, C
(TrEMBLrel. 17, I
(TrEMBLrel. 25, I
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124 GVAPPGFSIPEDG 136
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stigmatella aurantiaca
                                                                                                                        Thioredoxin-peroxidase
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SEQUENCE 144 AA; 1
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Q9A5K3;
01-JUN-2001 (
01-JUN-2001 (
01-OCT-2003 (
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QBRJY9;
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STRAIN=2603 V/R / Serctype V;
STRAIN=22222988; PubMed=12200547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBOY R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini B.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
EMBL; AEOL4194; AAM98961.1; TIGR; SAG0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                          44.8%; Score 47; DB 16; Length 880; 50.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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                                                            Pfam; PF00171; aldedh; 1.
Pfam; PF00465; Re-ADH; 1.
PROSITE; PS00913; ADH IRON 1; 1.
PROSITE; PS00060; ADH IRON 2; 1.
PROSITE; PS00060; ADH IRON 2; 1.
SEQUENCE 880 AA; 97005 MW; FC26D6B9F7FF384C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; F:metabolism; IEA.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001670; Fe-ADH.
Pfam; PF00171; aldedh; 1.
PROSITE; PS000913; ADH IRON_1; 1.
PROSITE; PS000913; ADH_IRON_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              880 AA
                                                                                                                                                                                                                                                                                                                                          3; Mismatches
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001670; Fe-ADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPALVMTVPGFIAADTGM 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aldehyde-alcohol dehydrogenase.
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Best Local Similarity 50.0°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 880 AA;
                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus.
NCBI_TaxID=216466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADHE OR SAG0053
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Search completed: March 22, 2004, 06:59:22
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MEDINE-21176699; PubMed=11259647;

MISCHAIN-ATCC 19089 / CE15;

MACHOLINE-21176699; PubMed=11259647;

MACHOLINE-21176699; PubMed=11259647;

MACHOLINE-21176699; PubMed=11259647;

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MACHORY N.T., Dodson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

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MACHORY J. A., Palanthevan J., Ellinghyll J.,

MACHORY J. Phydrolase activity; IEA.

MACHORY J. PRO06680; Anidohydrol.

MACHORY J. PRO06581; Anidohydrol.

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Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
Wing C.A., Collura K.;
"Rice Genomic Sequence.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC104473; AAN60993.1; -.
EMBL; AC104473; Pthydrolase activity, hydrolyzing O-glycosyl . .; IEA.
GO; GO:00064553; Pthydrolase activity; IEA.
GO; GO:0005975; Ptarbohydrate metabolism; IEA.
InterPro; IRR000499; Glyco_hydro_17.
Pfam; PP00332; Glyco_hydro_17; 1.
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01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
Putarive glycosyl hydrolase.
OJ1626B05.8.
OJ72A sativa (japonica cultivar-group).
Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                         Caulobacter crescentus.
Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales;
Caulobacteracea, Caulobacter.
NCBI_TaxID=155892;
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DD OTIGO
GN OCTIGO
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MEDLINE=21456156; PubMed=11572479; MEDLINE=21456156; PubMed=11572479; Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Antai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; APD00983; BAB65737.1;
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR00673; AMP-bind.
PF00501; AMP-binding; 1.
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Hypothetical protein; Complete proteome.
SEQUENCE 662 AA; 74544 MW; FC698FB9AEA2C107 CRC64;
                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative acetyl-CoA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 17;
Pred. No. 1.2e+02;
4; Mismatches 6;
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                              391 PSRGMTPTGYCVTAAGV 407
2 PAKGMSPPGFIVGEEGV 18
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Matches 8; Conservative
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us-09-662-293-13.rag

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

March 22, 2004, 06:30:23; Search time 6.08116 Seconds

(without alignments)
929.256 Million cell updates/sec

Title:

US-09-662-293-13

Perfect score:
105
Sequence:
1 DPAKGMSPPGFIVGEEGVLS 20

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107
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Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*
2: geneseqp290s:\*
4: geneseqp2001s:\*
5: geneseqp201s:\*
6: geneseqp2003as:\*
7: geneseqp2003as:\*
8: geneseqp2003bs:\*

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	10000	Describtion	Aay52513 House dus	Aay52522 House dus	7	Aau96326 Der HMW-m	Aay52535 D. pteron	5339 Der	Aay52533 D. pteron	7 Der	Aau96338 Der HMW-m	Aay52525 House dus	Aau96329 Der HMW-m	Aay52523 House dus	Aau96327 Der HMW-m		Abb68081 Drosophil	Aab58145 Lung canc	4 Wild	7 TNF r	Aay00934 Human DR5	Aaw76827 Human TR6	Aaw79083 Human dea	Aaw79261 Tumour ne	Aaw88410 Human Apo	Aaw83321 Human Apo	Aaw93576 Human hAP
SUMMARIES	£	TD	AAY52513	AAY52522	AAU96317	AAU96326	AAY52535	AAU96339	AAY52533	AAU96337	AAU96338	AAY52525	AAU96329	AAY52523	AAU96327	AAU96328	ABB68081	AAB58145	ABG71824	AAU99897	AAY00934	AAW76827	AAW79083	AAW79261	AAW88410	AAW83321	AAW93576
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Aaw93608 Human kil Aay00932 Human DR5 Aay55805 Human Apo Aab29790 Human dea	Human Human Human Human	Amino Human Amino Human Angiog	Abr58626 Human can Abr70904 Human FAM Aac29541 Human TRA Abg71903 Human TRA Abg74383 Human TRA Abg74383 Human TRA
AAW93608 AAY00932 AAY55805 AAB29790		ABG31490 AAU76947 AAB09602 AAM51080 ABU03488	
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#### ALIGNMENTS

RESULT 1

Sequences AAY5510-Y52522 represent proteclytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HWW-map) composition. The HWW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. The HWW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therepeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially fellnes, canines, equines, Mite allergen protein; map; high molecular weight; HWW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation. Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens. House dust mite allergen protein (map) A/B fragment map(3). Ş Claim 3; Page 69; 154pp; English. Weber ER; AAY52513 standard; peptide; 20 98US-00062013. 98US-0085295P. 98US-0098909P. 99WO-US008524. (first entry) Dermatophagoides farinae. Hunter SW, WPI; 2000-052700/04. (HESK-) HESKA CORP. 17-APR-1998; 13-MAY-1998; 02-SEP-1998; WO9954349-A2. 16-APR-1999; 22-FEB-2000 28-OCT-1999 Mccall CA, AAY52513; 

allergens from a mixture of proteins

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Dermatories Arithae high molecular weight mite allergen protein (HWW map) composition. The HWW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgB present in mite-allergic dog antisera. The HWW-map composition comprises mapA (a 109 kD protein) and may 108 kD kD. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, chier pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a proteins and peptides can also be used to raise antibodies, which have a passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite
humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; JgE; immunoglobulin B; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; canine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    House dust mite allergen protein (map) A/B fragment map(12).
                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                               100.0%; Score 105; DB 3;
100.0%; Pred. No. 3.1e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAYS2522 standard; peptide; 20 AA
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                                                                                                                                                                                                                                                                                                     DPAKGMSPPGFIVGEEGVLS 20
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98US-0085295P.
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                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                              Sequence 20 AA;
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13-MAY-1998;
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Libermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a non-proteinscenus epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the clerction of anti-Der HWW-map antibodies in animal fluids, and inhibition of immunoglobulin (1g)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgE, to prevent immunoscomplex formation, thus ceducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences ANU96314-AAU96342 represent Der HWW-map polypeptides of the invention
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Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                            Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;
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                                                        Score 105; DB 3;
Pred. No. 3.1e-09;
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                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                Der HMW-map polypeptide #4.
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                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                immunocomplex formation.
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                             Sequence 20 AA;
                                                          Query Match
Best Local Simi
Matches 20;
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115. 117 /note= "Asn is N-glycosylated" 240. 242 240. .242 /note= "Asn is N-glycosylated"

Location/Qualifiers

us-09-662-293-13.rag

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Mite allergen protein; map; high molecular weight; HWW-map; allergy; house dist mite; 1gE; immunoglobulin E; allergen; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; cannine; veterinary; antibody; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 147-149; 154pp; English.
                                                                                                    Dermatophagoides pteronyssinus.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-052700/04.
N-PSDB; AAZ38589, AAZ38590.
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                                                                                                                                            Modified-site
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02-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein is useful for eliciting an immune response proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunosibulin (ig)s or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to Igs, to prevent immunocomplex formation, thus reducing Mypersensitivity responses to mite allergens, and as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mite allergenic protein isolated from Dermatophagoides, designated Der HWW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                        Der HWW-map, American house dust mite; antiallergic; mite; IgB;
mite allergenic protein; immunoglobulin E; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                         AAU96326 standard, peptide, 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 71; 161pp; English
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                                                                                                                                              Der HMW-map polypeptide #13
                                                                                                                  (first entry)
                                                                                                                                                                                      mite allergenic protein; immunocomplex formation.
                                                                                                                                                                                                                                  Dermatophagoides farinae
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Best Local Similarity
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                             RESULT 4
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Weber ER;

Hunter SW,

98US-00062013. 99WO-US008524

98US-0085295P

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This sequence represents Dermatophagoides pteronyssius mite allergen

protein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490

thas a molecular weight of 98 kb, comprising 490 amino acids, and has a

high degree of homology with the D. fariane mature 98 kb allergen, mapB

CC (AAY52525). Nucleic acid molecules encoding PDerp98-490 were isolated

CF from a D. pteronyssius cDNA library by hybridisation with a probe

encoding the D. fariane high molecular weight map (HMW-map) composition.

Mite allergenic proteins and peptides, and nucleic acids encoding them,

may be used in therapeutic compositions to modify an animal s

cm pub be used in therapeutic compositions to modify an animal s

include mammals and birds, especially felines, canines, equines, humans,

cother pets, and work or domestic animals. The proteins or fragments may

also be used to diagnose allergies via a variety of

poptides can also be used to raise antibodies, which have a variety of

potential uses. For example, they can be used as vaccines to passively

in test kits and as cools to recover desired dust mite allergens from a

in test kits and as tools to recover desired dust mite allergens from a

mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
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Matches 19; Conservative
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AAU96339
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AAY52535 standard; protein; 490 AA.

(revised)
(first entry)

06-AUG-2003 22-FEB-2000

AAY52535;

RESULT 5
AAY52535
ID AAY5
XX
AC AAY5
XX
DT 06-A
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Dermatophagoides pteronyssinus.

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Dermatophagoides, designated ber How-map protein, and its related nucleic against the Der How-map protein. The protein are against comprising an immune response protein. The protein are against comprising a non-protein are part to make a reagant comprising a non-protein composition is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A cherapeutic composition is useful for idensifising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HWW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig) so IDer HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to Igs. to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mate allergen hypersensitivity. Sequences Adubé0314-AAU96312 represent Der HWW-map polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                               Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.2%; Score 101; DB 5; Length 490; 95.0%; Pred. No. 4.1e-07; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 144-146; 161pp; English.
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                                    Der HMW-map polypeptide #26
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(first entry)
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                                                                                                                                                 Dermatophagoides farinae
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N-PSDB; ABK69585.
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Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                      (HESK-) HESKA CORP.
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 15-JUL-2002
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22-FEB-2000
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This sequence represents Dermatophagoides pteronyssius mite allergen protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD, comprising 509 amino acids, and has a high degree of homology with the D. farinae 98 kD allergen, mapB (AAY5223). Nucleic acid molecules encoding PDerp98-509 were isolated from a D. pteronyssius cDMA library by homologic modification with a probe encoding the D. farinae high molecular weight map (HWW-map) composition. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vacines to passively immunise animals against mite they can be used as vacines to passively immunise animals against dust mite crover desired dust mite allergate animals and as tools to recover desired dust mite allergate from a mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens.
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                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588.
                                                                                    20. .509
/note= "Mature PDerp98-509"
                                                  1. .19
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 134-136; 154pp; English.
                              Location/Qualifiers
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98US-0085295P.
98US-0098909P.
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Best Local Similarity 95.0°
Matches 19, Conservative
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                                                                                        Protein
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16-APR-1999;
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02-SEP-1998;
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                                  Mccall CA,
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                                                                                                                                                                                                                                                              The invention relates to an isolated mite allergenic protein of bermatophagoides, designated ber HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against ber HWW-map protein. The protein or a reagant comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the allergic response to a mite. The DNA and protein can be used in the detection of anti-ber HWW-map antibodies in animal fluidas, and inhibition of immunoglobulin (Ig)E or ber HWW-map protein activity associated with a disease. Antibodies that bind to ber HWW-map are useful for inhibiting
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                                                                                                                                                                                                        New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                  Weber ER;
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                                                                               14-SEP-2001; 2001WO-US028730.
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                                                                                                    14-SEP-2000; 2000US-00662293
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les 19, Conservative
           Dermatophagoides farinae
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                                                                                                                                                 Hunter SW,
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                                                                                                                         (HESK-) HESKA CORP
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                                                                                                                                                                                 N-PSDB; ABK69581
                                  WO200222807-A2
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Best Local Si
Matches 19,
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Dermatophagoidee, designated Der HWM-map protein, and its related nucleic acid. The Der HWM-map protein is useful for eliciting an immune response acid. The Der HWM-map protein is useful for eliciting an immune response protein protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the clatection of anti-Der HWW-map and protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibition of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as a vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96312 represent Der HWW-map printennen
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                                                                                                                                                                                                                                                    mite allergenic protein isolated from Dermatophagoides, designated HMW-map protein, useful as a vaccine for treating mite allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     to an isolated mite allergenic protein of
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                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 139-141; 161pp; English
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                                                                      Weber ER;
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N-PSDB; AAZ38579, AAZ38580
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                                                                      Hunter SW,
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                                                                                                                                            WPI; 2002-351888/38.
(HESK-) HESKA CORP.
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Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens. Der HMW-map, American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; 14-SEP-2001; 2001WO-US028730 14-SEP-2000; 2000US-00662293 Dermatophagoides farinae immunocomplex formation. (HESK-) HESKA CORP Sequence 536 AA; WO200222807-A2. 15-JUL-2002 21-MAR-2002. AAU96329; 8 셤

Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response orid. The Der HWW-map protein. The protein or a reagent comprising a non-protein septemble to or a reagent comprising a non-protein septemble to or identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the cletection of anti-Der HWW-map artibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting in proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWW-map polypeptides of the invention AAY52523 standard; protein; 555 AA. 279 DPAKGMSPPGFISGEEGVLS 298 1 DPAKGMSPPGFIVGEEGVLS 20 Local Similarity 95.0 nes 19; Conservative Sequence 536 AA; AAY52523; Query Match Peptide Key AAY52523 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ ਨੇ 셤 This sequence represents Dermatophagoides farinae mite allergen protein

(map) Poerf98-536, the mature form of Poerf98-558 (ANYS223). PDerf98-536

has a molecular weight of 98 kD, comprising 536 amino acids, and is a

component of the Dermatophagoides farinae high molecular weight mite

allergen protein (HWM-map) composition. The HMW-map composition was

component of the Dermatophagoides farinae high molecular weight mite

CC allergen protein (HWM-map) composition. The HMW-map composition was

craction being analysed for the presence of proteins that bound to IgE

CC present in mite-allergic dog antisera. Mite allergenic proteins and

CC present in mite-allergic dog antisera. Mite allergenic proteins and

CC compositions to modify an animal's hypersensitivity reaction to mite

allergens. Animals that may be treated include mammals and birds,

CC compositions to modify an animal's hypersensitivity reaction to mite

allergies via a skin test. The proteins and peptides can also be used to

CT alse antibodies, with have a variety of potential uses. For example,

CT has an be used as vaccines to passively immunise animals against dust

CT recover desired dust mite allergens from a mixture of proteins ö Gaps ö Score 99, DB 3; Length 536; Pred. No. 9.1e-07; 0; Mismatches 1; Indels Claim 3; Page 125-127; 154pp; English AAU96329 standard; protein; 536 AA. 279 DPAKGMSPPGFISGEEGVLS 298 DPAKGMSPPGFIVGEEGVLS 20 94.3%; 95.0%; Der HMW-map polypeptide #16 (first entry) Query Match
Best Local Similarity 95.0
Matches 19; Conservative

. 0

Gaps

ö

Length 536,

94.3%; Score 99; DB 5; Length 536 95.0%; Pred. No. 9.1e-07; ive 0; Mismatches 1; Indels

Mite allergen protein; map; high molecular weight; HMW-map; allergy; house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB; hypersensitivity reaction; therapy; treatment; diagnosis; human; feline; This sequence represents Dermatophagoides farinae mite allergen protein (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD, Novel high molecular weight Dermatophagoides nucleic acid polypeptides used to modify an animals' hypersensitivy to mite allergens. House dust mite (D. farinae) mite allergen protein (map) PDerf98-555 canine; veterinary; antibody; vaccine; immunisation N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578. /note= "Mature PDerf98-555" 1. .19 /note= "Signal peptide" Claim 3; Page 111-113; 154pp; English. Location/Qualifiers Weber ER; 98US-0085295P. 99WO-US008524 98US-00062013 (first entry) Dermatophagoides farinae. . 555 Hunter SW, 2000-052700/04. (HESK-) HESKA CORP. 17-APR-1998; 13-MAY-1998; 02-SEP-1998; 22-FEB-2000 WO9954349-A2 16-APR-1999; Mccall CA, 28-OCT-1999 Protein 

New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.

Weber ER

Mccall CA, Hunter SW, 2002-351888/38

WPI; 2002-351888/ N-PSDB; ABK69575.

The invention relates to an isolated mite allergenic protein of

Claim 12; Page 125-127; 161pp; English.

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of immunoglobulin (Ig)E or Der HWW-map protein activity associated with disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to IgS, to prevent immunocomplex formation, thus reducing hypersensitivity response on mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HWW-map polypeptides of the invention

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Gaps

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Length 555; Indels

94.3%; Score 99; DB 5; I 95.0%; Pred. No. 9.5e-07;

0; Mismatches

Local Similarity 95.0 hes 19; Conservative

Sequence 555 AA;

8888888

Query Match Matches 298 DPAKGMSPPGFISGEEGVLS 317

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1 DPAKGMSPPGFIVGEEGVLS 20

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comprising 555 amino acids, and is a component of the Dermatophagoides farinae high molecular weight mite allergen protein (HWW-map) composition. The HWW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IgE present in mite-allergic dog antisera. Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins
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                                                                                                                                                                                                                                                                                                                       Length 555;
                                                                                                                                                                                                                                                                                                                     Query Match 94.3%; Score 99; DB 3; Length 555
Best Local Similarity 95.0%; Pred. No. 9.5e-07;
Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU96327 standard; protein; 555 AA
                                                                                                                                                                                                                                                                                                                                                                                                            298 DPAKGMSPPGFISGEEGVLS 317
                                                                                                                                                                                                                                                                                                                                                                                        1 DPAKGMSPPGFIVGEEGVLS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Der HMW-map polypeptide #14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                       Sequence 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200222807-A2
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AAU96327
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Der HMW-map, American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity;

Dermatophagoides farinae immunocomplex formation.

WO200222807-A2. 21-MAR-2002.

Der HMW-map polypeptide #15 15-JUL-2002 (first entry)

AAU96328 standard; protein; 555 AA

RESULT 14

AAU96328;

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The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a nonprotein susceptible to or having an allergic response to a mite. A therapeutic composition is useful for identifying an animal (e.g., dog, therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. A map antibodies in animal fluids, and inhibition of immunoglobulin (Ig) so Der HWW-map protein activity associated with a disease. Antibodies that bind to Der HWW-map are useful for inhibiting binding of proteins to Igs, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU963142 represent Der HWW-map polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mite allergenic protein isolated from Dermatophagoides, designated
Der HMW-map protein, useful as a vaccine for treating mite allergy.
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Weber ER;

Hunter SW,

Mccall CA,

(HESK-) HESKA CORP.

WPI; 2002-351888/38. N-PSDB; ABK69573.

14-SEP-2001; 2001WO-US028730. 14-SEP-2000; 2000US-00662293 Sequence 555 AA;

The invention relates to an isolated mite allergenic protein of bermatophagoides, designated ber HWW-map protein, and its related nucleic acid. The Der HWW-map protein is useful for eliciting an immune response against Der HWW-map protein. The protein or a reagent comprising a nonproteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HWW-map antibodies in animal fluids, and inhibition

New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.

Weber

Mccall CA, Hunter SW, WPI; 2002-351888/38.

N-PSDB; ABK69571

(HESK-) HESKA CORP

14-SEP-2000; 2000US-00662293

Claim 12; Page 114-116; 161pp; English.

Query Match

Length 555; DB 5; 94.3%; Score 99;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 31035; 21pp + Sequence Listing; English.
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                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 31035.
Best Local Similarity 95.0%; Pred. No. 9.5e-07;
Matches 19; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers EW;
                                                                                                                                                                                                                                                                                     ABB68081 standard; protein; 488 AA.
                                                                                                                        298 DPAKGMSPPGFISGEEGVLS 317
                                                                                     1 DPAKGMSPPGFIVGEEGVLS 20
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 40.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
N-PSDB; ABL12184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical.
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ABB68081
ID ABB
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Gaps

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407 DPOEGFDPPTYLIGPDEELS 426

1 DPAKGMSPPGFIVGEEGVLS 20

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